

APPROVED	FIG.
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FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

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FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEE
 KTLISKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTL
 KVCCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFS
 SLRNETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQECK
 NANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGCADVDECSLAEKTCVRKNENCYN
 TPGSYVCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide: amino acids 1-24

N-glycosylation sites: amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites:

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 26-30

Casein kinase II phosphorylation sites:

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259,
 295-299, 339-343 and 349-353

Tyrosine kinase phosphorylation site: amino acids 303-310

N-myristoylation sites:

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164,
 164-170, 252-258 and 313-319

Aspartic acid and asparagine hydroxylation site: amino acids
 308-320

EGF-like domain cysteine pattern signature: amino acids
 166-178

Leucine zipper pattern: amino acids 94-116

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FIGURE 3

CAGGTCCAACCTGCACCTCGGTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
 GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAAGGGGAACA
 GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
 GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTC
 CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
 CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
 TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
 TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC
 CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTGCCTCCCTGGATA
 AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
 TCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGGAACAGGATGGGGTGGCAGCATTTGAAGT
 GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTTCTCAAACACCTCAAAATGCTATCT
 TCTTTAAACATGTCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT
 GAAAGACGCATCTGCGAGTGTCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTG
 TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
 GATTCTATGGAGTGAACGTGACAAAGCAAACTGCTCAACCACCTGCTTTAATGGAGGGACC
 TGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
 CAAATGCCCACAACCCTGTGAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGTT
 CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT
 GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
 TAAAGGTACGAAGCCAGCCTCATACTATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
 ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTTTAAGTTACACCAAGTTCATAGCCTTTGTAAACCTTTCA
 TGTGTTGAATGTTCAAATAATGTTTACTTAACTTAAGAATACTGGCCTGAATTTTATTAGCT
 TCATTATAAATCACTGAGCTGATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAG
 CATGATGGTATAGATTTTCTTGTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
 TCAGGTTAAAATTTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTTACAATGCATTTATGGT
 GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT
 TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTCAGATATTTAGAT
 GTTTGTTACATTTTTTAAAAATGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACC
 TTACCATTATTCCAGAGATTGAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATT
 AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCA
 TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT
 ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
 CGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESELYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide: amino acids 1-28

N-glycosylation site: amino acids 88-92, 245-249

Casein kinase II phosphorylation site: amino acids 319-323

Tyrosine kinase phosphorylation site: amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature: amino acids

198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
 CCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACCATGTGCGGATGTCCAGTGGGGCTAC
 TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG
 GAGCTAGCACCGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
 GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
 GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
 TGCCTCGGCGTGCCACCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
 TCCAGTCTTGGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGT
 GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
 GAACCACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCATTCGCTACCGCCTGGGCACCA
 TCCGCCCATCTTCCTCGGTGATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG
 GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA
 CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
 CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCAGAACCTGCTGTCTTGTGAC
 ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTTGCCTCG
 CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
 CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC
 CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
 CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
 TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
 CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
 AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
 CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG
 AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCATCACTGAGGCTG
 CGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
 GGGCGGTGACCCCAGCCTCGCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
 CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
 GAGCCCCCAGACCTCCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
 ATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
 CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
 TTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACTCCGACTCCTGGGTTC
 AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC
 TAATTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAACT
 CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
 ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA
 TAAACCAAAGTATTGATAAAAAAAA

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDG

ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR

CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDGP

N-glycosylation site: amino acids 78-82, 161-165

Casein kinase II phosphorylation site: amino acids 80-84,
117-121, 126-130, 169-173, 205-209, 296-300, 411-415

N-myristoylation site: amino acids 21-27, 39-45, 44-50,
104-110, 160-164, 224-230, 269-275, 378-384, 442-448

Amidation site: amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site:
amino acids 398-409

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FIGURE 7

AGGCTCCTTGGCCCTTTTCCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACA@CCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCACTGCCCACTGE
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAAGATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

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FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPLRCSLHSACCSGDPASYRLWGAPLQPT
 LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSDT
 DPPADGPSNPLCCCFHGPAPFSTLNPVLRHLFPQEAFPAHPIYDLSQVSVVSPAPSRGQALR
 RAQ

Signal peptide: amino acids 1-47

N-glycosylation site: amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site: amino acids 22-26,
 76-80

N-myristoylation site: amino acids 56-60

Amidation site: amino acids 70-74

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FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHYQVVTGRRI
SATAEDGNKFACLIVETDTFGSRVRIKGAESEKYICMNKRGKLGKPSGKSKDCVFTEIVLE
NNYTAFQNAHEGWFMFAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide: amino acids 1-22

N-glycosylation site: amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 60-64

Casein kinase II phosphorylation site: amino acids 65-69

Tyrosine kinase phosphorylation site: amino acids 39-48,
89-97

N-myristoylation site: amino acids 69-75, 188-194

Amidation site: amino acids 58-62

HBGF/FGF family signature: amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
 CATA CGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCTCATCCAGT
 CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
 TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCT
 GAAGTCTTGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC
 TGGATTTCCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
 AATATTCAGACCATTTCACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC
 TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTGCATATCCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
 CACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT
 AAACCACATTTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCCTTGGTTTTGTGACTGCAGTATTAAATGGGTCACAGAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCCTGAACAAGTCCGGG
 GGATGGCCGTCAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTG
 CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT
 TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAACTTCCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCGTGATGGCATA
 CAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTTCAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC
 CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAATACAACCGGGGCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
 AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA
 CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
 ACTGCCATACGTTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACCTTTTGCTTTTTTAAATCTT

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FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLOENNIQTI
 SRAALAQLLKLEELHLLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
 PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARELNMNLLSCPTTTPGLPLFTP
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGRERVTPPISERIQLSIHFVND
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
 LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
 DFRLQPIIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide: amino acids 1-42

Transmembrane domain: amino acids 542-561

N-glycosylation site: amino acids 202-206, 298-302, 433-437,
 521-525, 635-639, 649-653

Casein kinase II phosphorylation site: amino acids 204-208,
 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site: amino acids 319-328

N-myristoylation site: amino acids 2-8, 60-66, 149-155,
 213-219, 220-226, 294-300, 522-528, 545-551, 633-639

Amidation site: amino acids 581-585

Leucine zipper pattern: amino acids 164-186

Phospholipase A2 aspartic acid active site: amino acids 39-50

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FIGURE 14A

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCTCG
 CCTCCCACGAGCGATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGAAGGAGG
 AAGACCCGGGTGGCTGCGCCCCCTGCCTCGCTTCCCAGGCGCCGGCGGCTGCAGCCTTGCCCC
 TCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATCCTCGGACAG
 ATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCTCTAGGGGCAG
 ACACGCTCGGACCCACCCGCAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAGCGGGCAG
 ACCTGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAG
 GAGTTCATCGTGGACATCTTGCAATTCTTGGACATTGGTCCTGATGTCACCCGAGTGGGCCT
 GCTCCAATATGGCAGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCG
 AGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGGGCACCATGACTGGGCTGGCC
 ATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGAGGGAGAA
 TGTGCCACGGGTGATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGG
 CTGCTAAGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTC
 AACACCTTGAAGTCCATTGGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTT
 CAGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGCACGGCCACATGTGCA
 GCACCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTGGCTCATACTGTGCAGG
 TGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAAGATCCAGGATCTGTGTGC
 CATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGT
 GCTACAGTGGCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCC
 TCAGAAAACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTG
 CCATGAAGGATTTGCTCTTAACCCAGATGAAAAACGTGCACAAGGATCAACTACTGTGCAC
 TGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCTACTACTGCCGCTGC
 CACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCACA
 GCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGCT
 CAGAAGGCTTCCTCATCAACGAGGACCTCAAGACCTGCTCCCGGTGGATTACTGCCTGCTG
 AGTGACCATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCCTGTCAGTGTCC
 TGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTGCAAATTTGGACTCTTGTGCTCTGG
 GGGACCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT
 GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTAT
 AGACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATAACGTGCGAGTGCTTGG
 AGGGATTCCGGCTCGCTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACC

_____ To Figure 14B

APPROVE	C.G. FIG.	
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FIGURE 14B

From Figure 14A

CACCATGGCTGCGAACACATTTGTGTTAATAATGGGAATTCCTACATCTGCAAATGCTCAGA
 GGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATTGACC
 TGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCTGGAAGCAG
 TTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCT
 CCAGTATTCCACACAGGTCCACACAGAGTTCCTCTGAGAACTTCAACTCAGCCAAAGACA
 TGA AAAAAGCCGTGGCCACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTG
 AAACACATGTTTGAGAGAAGTTTTACCCAAGGAGAAGGGGCCAGGCCCTTTCCACAAGGGT
 GCCCAGAGCAGCCATTGTGTTACCGACGGACGGGCTCAGGATGACGTCTCCGAGTGGGCCA
 GTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTGAGGAG
 GAACTACAAGAGATTGCCTCTGAGCCACAAACAAGCATCTCTTCTATGCCGAAGACTTCAG
 CACAATGGATGAGATAAGTGA AAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCG
 ATGGAAGACAGGACTCTCCAGCAGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCT
 GAGCCAGTCACCATAAATATCCAAGACCTACTTTCTGTTCTAATTTTGCAGTGCAACACAG
 ATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTTCCCATTC AACAAAAC
 CTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTTC
 CAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAG
 AATGGAAGCCCTGGAAAATCGCCTGAGATACAGATTGAAGATTAGAAATCGCGACACATTTGT
 AGTCATTGTATCACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTA
 AATCAATAATGTTGTGAAGTAAACAATCAGTACTGAGAAACCTGGTTTGCCACAGAACAAA
 GACAAGAAGTATACACTAACTTGTATAAATTTATCTAGGAAAAAATCCTTCAGAATTCTAA
 GATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAATATACTGTGGACA
 CAACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAAGTTT
 GCACAGTCTTACTTCTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTT
 ACCTTGATATATGTATATGGATGTATGCATAAAATCATAGGACATATGTACTTGTGGAACAA
 GTTGGATTTTTTATACAATATTAAAATTCACCACTTCAG

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FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFHI
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KRMRLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSTVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGLI
NEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSCALGDHGCE
HSCVSSDSFVCQC FEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCSTHHGCEHICVNNGNSYICKCSEGFLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQEGGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDS DGRQDS
PAGELPKTVQQPTESEPTVINIQDLLSCSNFAVQHRYLFEEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide: amino acids 1-23

N-glycosylation site: amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site: amino acids 49-53,
118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446,
501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823,
866-870

N-myristoylation site: amino acids 133-139, 258-264, 299-305,
340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

Amidation site: amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site: amino acids
253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546,
581-587

APPROVE	C.B. FIG.	
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FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCTGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

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FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
 SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLOEKDSGPY
 SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
 WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
 VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLTPWPKSSDTISKNGTL
 SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSRLPTTDGAHPQPISPIPGGVSSSSGLSR
 MGAVPVMVPAQSQAGSLV

Signal peptide: amino acids 1-29

Transmembrane domain: amino acids 245-267

N-glycosylation site: amino acids 108-112, 169-173, 213-217,
 236-240, 307-311

N-myristoylation site: amino acids 90-96, 167-173, 220-226,
 231-237, 252-258, 256-262, 262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTTCCACTTTG
TTGAATTGTTCCCTATACTCAAAATTGCACCAAGACACCTTGTCTCCCAAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAAATGTGAATGCAAACCTGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAATAAAACTTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTTCACCAACAGA
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACA
CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTC AACGGATATAGCTCTCAAAGTTTCTTTTTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTTTATATTATA
AGAGTATTGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACTTGAAAAAATAACATTTACATTAAAGTCATCGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGCATTTTGAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTTGCAATTTTGATGTCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTT
ACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG
TAGCCTATTTCTTGCTGAACTTGTTTTTCTTGTTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGGACTGCTACACTACTTCTTTTTTAGCTGCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTTTTTGCA
CAAGAATTTTTATATCTTTGGCTATCTAAGCCAGCCGTGGTAGTTGGATTTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAACCTTTATT
TGGAGTTTTATAGGACCAGCATGCCTAATCATTCTTGTTAATCTCTTGCTTTTGGAGTCAT
CATATACAAAGTTTTTTCGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCCCTCTCGGCACCACCTGGATCTTT
GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGC
TTTCCAGGGGATGTTCAATTTTTTTTATTCCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAAATGTCCCTGTTGTTTTGGATGTTTAAGGTAAACATAGAGAATG
GTGGATAATTACAACCTGCACAAAAATAAAAAATTCCAAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAATTATCCAATTATTACTACTAGACAAAAAGTATTTTAAATCAGTTTTTCT
GTTTATGCTATAGGAACTGTAGATAATAAGGTAAAATTATGTATCATATAGATATACTATGT
TTTTCTATGTGAAATAGTTCTGTCAAAAATAGTATTGCAGATATTTGGAAAGTAATTGGTTT
CTCAGGAGTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTAACACGAGAAGTATATGAA
TGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCTTTGAAACTAGTCC
CCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGA
ATATCAAACAGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACTGTTTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAAGAATTGAAGAAACACATTTTACCATTTTGTGAA
TTGTTCTGAACTTAAATGTCCACTAAAACAACCTTAGACTTCTGTTTGCTAAATCTGTTTCTT
TTTCTAATATTCTAAAAAATAAAGGTTTACCTCCACAAATTGAAAAAATAAAGGTTT
AAAAAATAAAGGTTTACCTCCACAAATTGAAAAAATAAAGGTTT

FIGURE 19

MKRLPLLVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
 GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCTAA
 NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
 SNSTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
 NSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLLYKSIQPLLS
 SSDNFLLPQNYDNSEEEERVVISVISMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
 WNYSPTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
 IISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIIAGL
 LHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
 TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA
 LALLFLLGTTWIFGVLHVHVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
 PCCFGCLR

Signal peptide: amino acids 1-19

Transmembrane domain: amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636, 648-664

N-glycosylation site: amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181, 188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site: amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site: amino acids 360-364

Casein kinase II phosphorylation site: amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154, 155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329, 346-350, 608-612

Tyrosine kinase phosphorylation site: amino acids 36-44, 669-677, 670-678

N-myristoylation site: amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394, 434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site: amino acids 75-87

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FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

APPROVED	FIG. 21	
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FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
 CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA
 CAAGAAGCCGCCGCTGCTGCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
 GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG
 CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACCTACAGCCCCGCAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
 ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
 ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGC
 CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGCCCATCAAGGG
 CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
 TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
 AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG
 GACCCATTTGGGCTTGTACCCGGAAGTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACT
 GAGACCATGCCCCGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGATACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
 CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA
 GGTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
 TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
 CTGAGGCCAGTTCTGTGATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC
 TTCCATCTCCCAGCCCACCAGCCCTCTGCCCACCTCACATGCCTCCCCATGGATTGGGGCCT
 CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
 TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
 CCTTTCCCCAGCACTTGGTTCCTAACATGATATTTATGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATTTATGTATGTAAGTGAGGTTTG
 TTTTGTATATTAAAATGGAGTTTGTTTGT

APPROVED	FIG. FIG.	
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FIGURE 22

MRS GCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALTVAIKGVH SVRYLCMGADGKMQGLLQYSEEDCAFE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide: amino acids 1-22

Casein kinase II phosphorylation site: amino acids 78-82,
116-120, 190-194, 204-208

N-myristoylation site: amino acids 15-21, 54-60, 66-72,
201-207

Prokaryotic membrane lipoprotein lipid attachment site: amino
acids 48-59

APPROVED	E.G. FIG.	
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FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCCGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACTGGAAGT
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

APPROVED	FIG.	
CLASS	SUBCLASS	
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FIGURE 24

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
 WKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGONLEED
 TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
 NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNNSVGYRRCPGKRMQVDDLNISGIIAAVVVVA
 LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGO
 EF

Signal peptide: amino acids 1-20

Transmembrane domain: amino acids 130-144, 238-258

N-glycosylation site: amino acids 98-102, 187-191, 236-240,
 277-281

Casein kinase II phosphorylation site: amino acids 39-43,
 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site: amino acids 182-188, 239-245, 255-261,
 257-263, 305-311

Amidation site: amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
 AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCCGACCCTGGCAT
 CATGCTGCTATTCTTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTGTAAATAA
 ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
 TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTGGACAATG
 CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTCATCA
 TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAAGTTACTAGCACTGACTG
 TGGAAATCCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
 CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
 TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
 ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCCAGCCAGATTGCC
 AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
 ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT
 ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA
 ACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCACTTACAAGAACTCTATATTAATCACAAC
 TGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
 AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT
 TCTGATGATTGGGGAAAAATCCAATTATCAGAATCAAAGACATGAAGTTAAGCCTCTTATCA
 ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
 GGACTGGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
 TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTGGATCTAAATAAAAATCCTATTAATAGAA
 TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCT
 GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
 TACTAACAAACCCTAGATTGTCTTACATTACCCCAATGCATTTTTCAGACTCCCCAAGCTGG
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
 CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTATCCGTTG
 GATGAACATGAACAAAACCAACATTTCGATTTCATGGAGCCAGATTCAGTGTGCGTGGACC
 CACCTGAATTCCAAGGTCAGAATGTTGGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT
 CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
 TTCTTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
 GTCAAAAACCTTGCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
 GATATAAATGGCGTAACCTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT
 TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
 GCTCTTTGAATATTAAAAATAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCTCTGGAAAGCA
 AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA
 TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
 CATCAACTGAGTATAAAATTTGTATTGATATTTCCACCATCTATCAGAAAAACAGAAAAAA
 TGTGTAAATGTCACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
 CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
 GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
 AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
 AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCAAGGAAACCTACTCCAAAAATGAAC

APPROVED	FIG.	
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FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
 FPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQELSVYLE
 ENKLTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
 LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
 IKVPHVALQKVVNLKFLDLNKNPINRIRRGDFSNNLHLKELGINNMPELISIDSLAVDNLPD
 LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNIRC
 DCVIRWMMNMKTNIRFMEPDSLFCVDPPEFQGQNVVRQVHFRDMMEICLPLIAPESFPSNLNV
 EAGSYVSFHCRTAEAPQPEIYWITPSGQKLLPNTLTDFYVHSEGLDINGVTPKEGGLYTC
 IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
 KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
 YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLIN
 LWEGKEKSTSLKVKATVIGLPTNMS

Signal sequence: amino acids 1-22

Transmembrane domain: amino acids 633-650

N-glycosylation site: amino acids 93-97, 103-107, 223-227,
 382-386, 522-526, 579-583, 608-612, 624-628, 625-629

Casein kinase II phosphorylation site: amino acids 51-55,
 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site: amino acids 570-579

N-myristoylation site: amino acids 13-19, 96-102, 158-164,
 221-227, 352-358, 437-443, 491-497, 492-498, 634-640, 702-708

Cell attachment sequence: amino acids 277-280

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FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCCAAAATCAGGAG
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATTAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTTCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAA
ACA

APPROVED	FIG.	
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FIGURE 28

MNLVDLWLTRSLSMCLLLQS FVLMILCFHSASMCPKGCLC SSSGGLNVTCSNANLKEIPRDL
 PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR
 IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
 NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVYYYVRQNQEDARRHLEYLKS LPSRQKK
 ADEPDDISTVV

Signal sequence: amino acids 1-33

Transmembrane domain: amino acids 205-220

N-glycosylation site: amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 199-203

Casein kinase II phosphorylation site: amino acids 162-166,
 175-179

N-myristoylation site: amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
 GGCGTGAGGAGCATGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
 GGGCTCAGTGCTGTGTCAGGCTCGGCCACGGGCTGCCCCCGCTGCGAGTGCTCCGCCCAGG
 ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
 ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
 CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCG
 CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
 CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
 CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
 ACAATGACCTCGTCTACATCTCTCACC GCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
 ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
 CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
 TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
 TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
 CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCCTACAACCCCATCA
 GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
 GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
 TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
 AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
 CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCAGTTTGTCCA
 GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACCTGCCGCCGCG
 CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
 GTGTGCCGGGCGGATGGCGACCCGCCGCCGCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT
 GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
 ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
 TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA
 GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
 TGCCTTTCCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
 CTGGGCGTCGTCTTCTGCTGGTGCTGCTGTTTCTCTGGAGCCGGGGGCAAGGGCAACAC
 AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
 ACGCGCCCCGCAAGTTCAACATGAAGATGATATTGAGGCGGGGCGGGGGGAGGGACCCCCG
 GGCGGCCGGGCGAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCCAGTCTTCCCACCTC
 CTCCCTACCTTCTACACACGTTCTCTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG
 CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA
 CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
 ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTT
 TATGAAAACCTTGAAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

APPROVED	G. FIG.	
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FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVVGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNERTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLT SIPTEALSHLHGLIVLRRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSI THCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSM LHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFH SVGNLET LILDSNPLA
CDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGR LTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGND SMPAHLHVSYS PDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence: amino acids 1-41

Transmembrane domain: amino acids 556-578

N-glycosylation site: amino acids 144-148, 202-206, 264-268,
274-278, 293-297, 341-345, 492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site: amino acids 49-53,
108-112, 146-150, 300-304, 348-352, 349-353, 607-611

Tyrosine kinase phosphorylation site: amino acids 590-598

N-myristoylation site: amino acids 10-16, 32-38, 37-43,
113-119, 125-131, 137-143, 262-268, 320-326, 344-350, 359-365,
493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site: amino
acids 32-43

APPROVED	C. FIG.	
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FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCCGGGATTTCAGGCTCGCCAGCGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTTCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCCTGGTGGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAGA
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG
CTCATCATGCTCATCTTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTAGAGGCGCCTGCCCACTTCCTGC
GGCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTTACAGAGCAA
CCGCAGGGCCGCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCCGTGGCTTCTCTGCATTTGGGTATTATTATTTTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA
AACAAAAACA

APPROVED	C.G. FIG.	
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FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
 SNPAQQTLYFGEKRALRDNRILQVLTSTPHELSISISNVALADEGEYTCSI FTMPVRTAKSLV
 TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
 TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGO
 KLLLLHCEGRGNPVPQQYLWEKEGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
 YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLI FLGHYLRHKGTYLTHEAKGSDD
 APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence: amino acids 1-20

Transmembrane domain: amino acids 331-352

N-glycosylation site: amino acids 25-29, 290-294

Casein kinase II phosphorylation site: amino acids 27-31,
 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site: amino acids 2-8, 23-29, 156-162,
 218-224, 295-301, 298-304, 306-310, 334-340, 360-364, 385-389,
 386-390

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTTTCCTGG
 CTTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTTCGCTG
 TTACTTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
 GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAAGAGAAGA
 TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
 AGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTTACCATTTATTTCTGCAATGGCAATTC
 CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
 AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG
 CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
 TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
 ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC
 GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
 CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
 GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC
 CTGATCGGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
 CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
 CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
 GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
 CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA
 GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCAGGGTCGGGTTTAAAGATGAAC
 TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
 GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
 ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAAG
 AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
 GAAATTCGCGGGGCTGCAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
 TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTTCTAACAACAACCTG
 CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTCGCTCTCTAAACTCAGCTGCACAA
 CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
 TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
 GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
 TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
 CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTGGCGGAGACCGGGACGCACTCC
 AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
 GTTTGTACCTCCGCCTTACCCTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC
 GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT
 GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
 TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
 ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG
 CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT
 GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
 GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCAGCACGACCCTGCTGGAAG
 AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCCTGTGGGGTTGGATGCCGCGGTTCTATAC
 ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG
 CCCCCTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
 TGTAATAAGTAACTTTGACTTCTGAC

APP'D	FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
 LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
 TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPIITHLDLRG
 NRLKTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
 GKDLNETTEQDLCPKLRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK
 IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHIPGSGLKMNCCNNRVSSSLADEKP
 KLSNVQELFLRDNKHHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
 LDTLSREKFAGLQNLLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
 SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKC
 ETPVNFRRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
 VPGLLLVFVTSFTVVGMLVFILNRKRKRDRDANSASEINSLQTVCDSSYWHNGPYNADG
 AHRVYDCGSHSLSD

Signal sequence: amino acids 1-15

Transmembrane domain: amino acids 618-638

N-glycosylation site: amino acids 18-22, 253-257, 363-367,
416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 122-126, 646-650

Casein kinase II phosphorylation site: amino acids 30-34,
180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661,
666-670, 693-697

N-myristoylation site: amino acids 17-23, 67-73, 100-106,
302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604,
603-609

Prokaryotic membrane lipoprotein lipid attachment site: amino
acids 337-348

APPROVED	FIG.	
9/	CLASS	SUBCLASS
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FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAACTGTTGGC
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCTCAG
AGAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGGCGG
CGGCGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCGCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTAGTAACATCTATTCTGAGATTCTTCGATGGGGAT
CACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAGCTCTGCTTTCACGAAAGCCCCTCTTCCCAGCCA
AGGAAGGAGTCTATGGGCCCCGCCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCCTTGCTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAAACCAAGAGGAACTTAC
TTGTGTAAGTACAAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTTCGGAGAA
TTTGAGAAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTAT
ATTGGTTTCGAAATCCCAGGGAAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

APPROVED	O.C. FIG.	
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FIGURE 36

MRPAFALCLLWQALWPGPGGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCTIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence: amino acids 1-16

Transmembrane domain: amino acids 399-418

N-glycosylation site: amino acids 189-193, 381-385

Glycosaminoglycan attachment site: amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 98-102, 434-438

Casein kinase II phosphorylation site: amino acids 275-279,
288-292, 342-346, 445-449

N-myristoylation site: amino acids 30-36, 35-41, 58-64,
59-65, 121-127, 151-157, 185-191, 209-215, 267-273, 350-356,
374-380, 453-459, 463-469, 477-483

Aspartic acid and asparagine hydroxylation site: amino acids
262-274

APPROVED	O.G. FIG.	
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FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
AACTGCCTACAACACAGAACAGCCTGTCACCACCACATTCCCTGTAACCACGGGTTTAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAACAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTC
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTTAGAAGTGCAATATTTATAGT
GTTATTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGC GTTTTCTA
AATCAATGCTTAATAAAATATTTTTTAAAGGAAAAAAAAAAAA

APPROVED	D.C. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 38

M R G A N A W A P L C L L L A A A T Q L S R Q Q S P E R P V F T C G G I L T G E S G F I G S E G F P G V Y P P N S K C T W K
I T V P E G K V V V L N F R F I D L E S D N L C R Y D F V D V Y N G H A N G Q R I G R F C G T F R P G A L V S S G N K M M V
Q M I S D A N T A G N G F M A M F S A A E P N E R G D Q Y C G G L L D R P S G S F K T P N W P D R D Y P A G V T C V W H I V
A P K N Q L I E L K F E K F D V E R D N Y C R Y D Y V A V F N G G E V N D A R R I G K Y C G D S P P A P I V S E R N E L L I
Q F L S D L S L T A D G F I G H Y I F R P K K L P T T T E Q P V T T T F P V T T G L K P T V A L C Q Q K C R R T G T L E G N
Y C S S D F V L A G T V I T T I T R D G S L H A T V S I I N I Y K E G N L A I Q Q A G K N M S A R L T V V C K Q C P L L R R
G L N Y I I M G Q V G E D G R G K I M P N S F I M M F K T K N Q K L L D A L K N K Q C

Signal sequence: amino acids 1-23

N-glycosylation site: amino acids 355-359

Casein kinase II phosphorylation site: amino acids 64-68,
142-146, 274-278

Tyrosine kinase phosphorylation site: amino acids 199-208

N-myristoylation site: amino acids 34-40, 35-41, 100-106,
113-119, 218-224, 289-295, 305-311, 309-315, 320-326, 330-336

Cell attachment sequence: amino acids 149-152

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FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGTTCTT
 CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGGCCCCATGGCCCCCGAAGG
 GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
 CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACCTG
 CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACFTTGAG
 GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
 GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
 GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC
 AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGC
 CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
 GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
 AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
 TTTGGCCCCGTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
 CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
 GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
 GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
 GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
 ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
 ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
 AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
 CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
 ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATTA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
 TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG
 CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
 CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
 ATTTCAAAGTTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
 GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
 TCTGTGTTACACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
 AAGGTCTTGAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA

APPROVED	G.G. FIG.	
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FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGP EESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG
IIICALATLA AKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGF I KGR

Signal sequence: amino acids 1-29

Transmembrane domain: amino acids 372-395

N-glycosylation site: amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 290-294

Casein kinase II phosphorylation site: amino acids 63-67,
73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site: amino acids 8-14, 51-57, 59-65, 69-75,
70-76, 167-173, 173-179, 177-183, 188-194, 250-256, 253-259,
267-273, 280-286, 283-289, 326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site: amino acids
321-333

EGF-like domain cysteine pattern signature: amino acids
181-193

APPROVED	D.C. FIG.	
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DRAFTSMAN		

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FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
 GCACCATGCAGCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCCTGGCCAGCCCCGGG
 CCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
 GCCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCCAGT
 ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAGAGC
 TTCCGAGAGGTGGCCGGCAGGTTCCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
 CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
 AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC
 CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
 CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
 ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
 GAGCATCTGGGCCCCGTGGCGTCCGGCGCCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC
 GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG
 CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
 ATGTACATTGACCTGCAGGGGATGAAGTGGGCGGAGAACTGGGTGCTGGAGCCCCGGGCTT
 CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC
 CGTTTCTGGGGCCTCGACAGTGCATCGCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
 ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA
 GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGGCGCCTAGTG
 TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG
 GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
 CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
 GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT
 GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCCANTGTGTCATTGTTTACTTGTCTGTAC
 TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
 TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAACATGAATAAAACACATTTTATTCT
 AAAA

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FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
 ALLQRSHGDRSRGKRFSQS FREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLTFQEP
 VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRVSVHESGWKAFDNTTEAVNF
 WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLTLG DYGAQ
 GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEAFAFKWPF
 LGPRQCIASETDSLPMIVSIEGGRTRPQVVS LPMNRVQKSCASDGALVPRRLQP

Signal sequence: amino acids 1-18

N-glycosylation site: amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 76-80

Casein kinase II phosphorylation site: amino acids 68-72,
 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site: amino acids 19-25, 156-162, 225-231,
 260-266, 274-280

Amidation site: amino acids 74-78

TGF-beta family signature: amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTGTCATCGTGGCAGCCGTCTTGTAACCCTGATTCTCCTGGGAAT
CTTGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTCTGGTGTGAGCCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAAGTTGTTTAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCCTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAACCGCTGCTCTAAAGAAAAGAAAAGTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

APPROVED	C.R. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW
KFDQGDTRRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTGMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence: amino acids 1-27

Transmembrane domain: amino acids 238-255

N-glycosylation site: amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 270-274

Casein kinase II phosphorylation site: amino acids 34-38,
82-86, 100-104, 118-122, 152-156, 154-158, 193-197, 203-207,
287-291

N-myristoylation site: amino acids 105-111, 116-122, 158-164,
219-225, 237-243, 256-262

APPROVED	FIG. FIG.	
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FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
 CGGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
 GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCAGGCCCGAGCTCAG
 GCTCGTGGCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCGCTCACCTGG
 CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
 ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCTGCACCGGCGTCA
 GTGACTGCTCTGGGGGAAGTACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
 GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
 CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
 GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
 ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC
 CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
 TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
 CTCCGCCCCTGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC
 CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
 GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
 CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
 TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG
 GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
 CCCCCTCTGAGGGTGGCGATTAAAGTTGCTTC

APPROV	AC. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
 TSGLCVPLTWRCRDLDCSDGSDEEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
 RNC SRLACLAGELRCTLSDDCIPLTWRC DGHPCPDSSDELGCGTNEILPEGDATTMGPPVT
 LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLV TATLL
 LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence: amino acids 1-30

Transmembrane domain: amino acids 230-246

N-glycosylation site: amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site: amino acids 84-88,
 140-144, 161-165, 218-222

N-myristoylation site: amino acids 3-9, 10-16, 26-32, 30-36,
 112-118, 166-172, 212-218, 224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 44-55

Leucine zipper pattern: amino acids 17-39

APPROVED	FIG. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
 GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCGACAGA
 CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
 GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
 GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
 CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
 GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
 GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA
 TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
 ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGG
 TACCCCGACCTACACAATATGGTTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
 CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
 TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
 GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
 CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTTCGTCT
 GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT
 GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTC
 TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCCTCCTGA
 CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
 CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
 TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
 ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
 GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
 CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
 GTCTGTATTACCTCCCAGGTGCCAAGAGAGACCCACCCTGCTTCGGACAACCCTGACATA
 ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT
 GTTGTTCCTAAGAAACTGATTGATTAAAAAATTTCCCAAAGTGTCTCTGAAGTGTCTCTTCAA
 ATACATGTTGATCTGTGGAGTTGATTCCTTTCTTCTCTTGGTTTTAGACAAATGTAAACAA
 AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
 CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
 PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
 PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLELAS
 SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
 PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
 WPSTHETLLTTWKIVAFTATSVLLVLLLVLARMFQTKFAHFPPRGPPRSSSSDPDEFVVD
 GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
 VSGSSELLQSLYSPPRCQESTHPASDNPDI IASTAEVASTSPGIHHAHWVFLRN

Signal sequence: amino acids 1-41

Transmembrane domain: amino acids 325-344

N-glycosylation site: amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site: amino acids 8-12,
 146-150, 252-256, 270-274, 313-317, 362-366, 364-368, 380-384,
 467-471, 468-472

N-myristoylation site: amino acids 4-10, 61-67, 169-175,
 203-209, 387-393, 418-424, 478-484

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 394-405

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FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA
 TGCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT
 AGCGCCCGAGTGTGCGGGGGGCGCACCCGAGTTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
 CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCCTGCTGAGTGCC
 TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA
 TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
 GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
 AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
 GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
 CACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTTCATG
 TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCCCTACATGTTCCAGTGGAATGATGA
 CCGGTGCAACATGAAGAACAATTTCAATTTGCAATATTCTGATGAGAAACCAGCAGTTCCTT
 CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
 GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
 CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT
 GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAAGCAACACACCATC
 TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
 AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATTCAGAGTGTGTT
 CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
 GAAAGTGGGTTTGTGACTCTGGTGAGCGTGAGAGTGGATTTGTGACCAATGACATTTATGA
 GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
 GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
 CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
 GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
 CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA
 GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
 GCAGTGATAAAGATGGGCTGTGGAGCTTGAAAACACCTCTGTTTTCTTCTGCTCTATACAG
 CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCA
 CAGGTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAA
 AGAGCAGGAAAAAAA

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FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
 NFEEAKEACRRDGGQLVSI ESEDEQK LIEKF IENLLPSDGD F WIGLR RREEKQSNSTACQDL
 YAWTDGSI SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
 SDEKPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREAAALNLAYILIPSIPLLLLLLV
 VTTVVCVWVICRKRKREQDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
 KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
 GWVENEIYGY

Signal sequence: amino acids 1-21

Transmembrane domain: amino acids 235-254

N-glycosylation site: amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 296-300

Casein kinase II phosphorylation site: amino acids 28-32,
 30-34, 83-87, 100-104, 214-218, 222-226, 299-303, 306-310,
 323-327

N-myristoylation site: amino acids 18-24, 37-43, 76-82,
 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
 ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
 GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCAATGATCACTGGTGT
 GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
 AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTTCGACCGCAGC
 CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
 GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC
 AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
 CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
 GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
 TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTTCGGAATCTG
 GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGACCCATCATCAT
 CCACACTGATGAAGCAGATTGAGAAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA
 GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
 AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
 GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
 CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
 GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
 CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGGCTCATGATG
 TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
 GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
 TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
 TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
 ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
 TTAAAATAAAGTGCCTTTATACAATG

APPROVED	G.C. FIG.	
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FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMOVVFRHGAR
 SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
 TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFOCQKE
 GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
 FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLOMAVGPFHILES
 NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
 FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Signal sequence: amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 218-222

Casein kinase II phosphorylation site: amino acids 87-91,
 104-108, 320-324

Tyrosine kinase phosphorylation site: amino acids 280-288

N-myristoylation site: amino acids 15-21, 117-123, 118-124,
 179-185, 240-246, 387-393

Amidation site: amino acids 216-220

Leucine zipper pattern: amino acids 10-32

Histidine acid phosphatases phosphohistidine signature: amino
 acids 50-65

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FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCTG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGCTTGTCTAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACATACATCA
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

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FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence: amino acids 1-15

Casein kinase II phosphorylation site: amino acids 47-51,
97-101, 115-119, 209-213, 214-218, 234-238, 267-271, 294-298,
316-320, 336-340

N-myristoylation site: amino acids 29-35, 43-49, 66-72,
68-74, 72-78, 98-104, 137-143, 180-186, 263-269, 286-292

Amidation site: amino acids 196-200

Speract receptor repeated domain signature: amino acids
29-67, 249-287

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FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
 CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
 GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTGGGCTGCCTGGG
 CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
 TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAGTCTTCTATGCT
 GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
 ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
 TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
 GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
 TGTGGACAAGAGGGTTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
 TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG
 ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
 CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
 TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
 ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
 GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
 CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
 AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
 TTA CTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
 AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
 AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
 AAAA ACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
 AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTA
 C

APPROV.	C.D. FIG.	
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FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
 KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
 VNNAGISYRGTIMDTTVDDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
 PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
 AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence: amino acids 1-21

Transmembrane domain: amino acids 104-120, 278-292

N-glycosylation site: amino acids 228-232

Glycosaminoglycan attachment site: amino acids 47-51

Casein kinase II phosphorylation site: amino acids 135-139,
 139-143, 253-257

Tyrosine kinase phosphorylation site: amino acids 145-153,
 146-153

N-myristoylation site: amino acids 44-50, 105-111, 238-244,
 242-248, 291-297

Amidation site: amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 6-17

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FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
 AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
 GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
 CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
 TTTTATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
 TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
 ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
 CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
 AAGCGCAATTAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA
 ATAGTGCCAGAATTTTAATGTTTGAACCTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
 TCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCCTTTAGCCAAAAGCTGATT
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
 CAAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
 AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTTGATTGCACTTAAATTTTGT
 ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
 TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
 ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
 AA
 AA

APPROVED	S.D. FIG.	
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FIGURE 58

MKFLLDIILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
 LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
 YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
 SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKPNPSTSLGPTLEPEEVNRLMH
 GILTEQKMFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence: amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 30-34, 283-287

Casein kinase II phosphorylation site: amino acids 52-56,
 95-99, 198-202, 267-271

N-myristoylation site: amino acids 43-49, 72-78, 122-128,
 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
 AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGTTGGTGCCATGTGGAAGGTGATTG
 TTTTCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
 GTTTCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
 TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGA
 AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
 TTTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
 AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTACAAGTAACATGA
 CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
 GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
 AGCACGGGATTTATACAGTGCACATAATTGAGTTTTTCCAGATATTTCTGAATATAAAAAATA
 ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
 ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
 TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
 TGTGGATGAGAAGCAAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
 AGGAAGCAGAAGTGGTTTGGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
 AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
 GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA
 GCCATCCACGTGGGGAATCAGACTTTTAAATGATGGAACATAGTTGAAAAGTACTTGCGAGA
 AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
 TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
 ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAA
 ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGAATTCATCAGGTAATTATTC
 GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
 TTCATTTATGGAAGGATGGGATCCTTATGTTGGATTAAACTACCTTCCCAAAGAGAACAT
 CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAA
 TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAATTATCCTTGAAACAAGTGAGC
 TTTTGTTTTTGGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
 TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
 AATTTTAGGGTCTTGAATAGGAAGTTTTAATTTCTTCTAAGAGTAAGTGAAGGTGCAGTTG
 TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
 GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
 TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAAT
 AAAATATTATATATAAAAGTAAAAA

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FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKIQKGRELSL
VGPFPG LNMKSYAGFLTVNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVT SNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALI QF
FQIFPEYKNND FYVTGESYAGKYVPAIAH LIHSLNPVREV KINLNGIAIGDGYSDRESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKA EKKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence: amino acids 1-22

N-glycosylation site: amino acids 81-85, 132-136, 307-311,
346-350

Casein kinase II phosphorylation site: amino acids 134-138,
160-164, 240-244, 321-325, 334-338, 348-352, 353-357, 424-428

Tyrosine kinase phosphorylation site: amino acids 423-432

N-myristoylation site: amino acids 22-28, 110-116, 156-162,
232-238

Serine carboxypeptidases, serine active site: amino acids
200-208

Crystallins beta and gamma 'Greek key' motif signature: amino
acids 375-391

APPROVED	D.G. FIG.	
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FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
 TTTTCCCTTTTCTAACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTTCTT
 GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
 CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
 TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
 CTGGGGGAGGGCCTGCCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
 AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
 TGAACCTAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
 TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
 GACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGGGAGAAAGTATGTTAAAAATA
 GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTC
 AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTTGGTCTGACCACTCTGCCTTGTGTTTT
 GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
 CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
 ACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
 ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
 CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
 ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
 CCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCCCTCACCAACAATGTCAACAAGCTGCT
 CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
 AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
 CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
 TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA
 GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
 TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT
 CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCCGAGA
 CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
 CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
 CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
 AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
 CAGTATCACCAACCGCCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT
 GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
 TGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
 CTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
 CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG
 TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
 ATTCACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
 GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTTAATTTTGTG
 ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
 TTTCAATATTTCCCAAACCTTAAGAAAAAAGCTTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
 RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
 YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNVVKLLIIDYSENRLACGSL
 YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
 FPTLSSRKLPDPPESSAMLDYELHSD FVSSLIKIPSDTLALVSHFDIFYIYGFA SGGFVYFL
 TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAA YLAKP
 GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFP IRAINLQIKERLQSCYQEGN
 LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
 YSVVFVGTKSGKLKKVRVYEFRC SNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence: amino acids 1-32

Transmembrane domain: amino acids 71-87

N-glycosylation site: amino acids 130-134, 145-149, 217-221,
 381-385

Casein kinase II phosphorylation site: amino acids 139-143,
 229-233, 240-244, 291-295, 324-328, 383-387, 384-388, 471-475,
 481-485, 530-534

N-myristoylation site: amino acids 220-226, 319-325, 353-359,
 460-466, 503-509

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FIGURE 63A

AGGCTCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAA
 CACGCGATGACCACGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGGACTCCTGCTGCT
 GGTGCTCTTGGGCTTCCTGGTGCTCCGCAGGCTGGACTGGAGCACCTGGTCCCTCTGCGGC
 TCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGAACCTCATGCTGGAGGATTCCACC
 TTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCCAGGGAGTACTGGAGGGACCG
 CCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACTGCT
 ATGAGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTG
 ATGGCCGCAGAGATCGGGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGAT
 GGACCTCGGGGGCTTGCCCAGCTGGCTACTCCAAGACCCTGGCATGAGGCTGAGGACAACTT
 ACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACCTGATGTCCAGGGTGGTGCCA
 CTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATGGTTCCTA
 TAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGG
 AACTGCTCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTG
 GCCACCATCAACTTGCAGTCAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGT
 CCAGGGGACTCAGCCCAAGATGGTGATGGAGTACTGGACGGGGTGGTTTGACTCGTGGGGAG
 GCCCTCACAATATCTTGATTCTTCTGAGGTTTTGAAAACCGTGTCTGCCATTGTGGACGCC
 GGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATGGAGC
 CATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAG
 AAGCCGGCGATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGC
 ATCCCTCTCCCTCCCCACCTGACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGT
 CTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACCTGGGGGAGCCAATCAAGTCTGAAAAGC
 CCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCTTCGGGTACATTCTC
 TATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGGT
 GTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCC
 TGATCCAGGGTTACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGG
 GAGAATATTGATGACCAGCGCAAAGGCTTAATTGGAAATCTCTATCTGAATGATTACCCCT
 GAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGAGCTTCTTTCAGAGGTTTCGGCCTGG
 ACAAATGGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTCTTGGGTAGCTTGTCC
 ATCAGCTCCACGCCTTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATT
 CATCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAGAAGACGCTTTACCTCC

_____ To Figure 63B

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FIGURE 63B

From 63A

CAGGTCCCTGGTTGAGCAGCGGAATCAACCAGGTCATCGTTTTTTGAGGAGACGATGGCGGGC
CCTGCATTACAGTTCACGGAAACCCCCACCTGGGCAGGAACCAGTACATTAAGTGAGCGGT
GGCACCCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTCCTCTTGACCTGAAGCCTGGTG
GCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGGACTGGGGG
CTACAGTCTGCCCCTGTCTCAGCTCAAAACCCTAAGCCTGCAGGGAAAGGTGGGATGGCTCT
GGGCCTGGCTTTGTTGATGATGGCTTTCTACAGCCCTGCTCTTGTCGCGAGGCTGTCGGGC
TGTCTCTAGGGTGGGAGCAGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTG
AAACGTGCCCTTGCACCGGACGTCACAGCCCTGCGAGCATCTGCTGGACTCAGGCGTGCTCT
TTGCTGGTTCCCTGGGAGGCTTGGCCACATCCCTCATGGCCCCATTTTATCCCCGAAATCCTG
GGTGTGTCACCAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTTCTTCC
TTCACAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGAC
TTCCCCTTTCCCTTCCCCTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGA
AATCCTCACCTGCGTCTTCCAAGTTAGCAGGTGTCTCTGGTGTTCAAGTGAAGGAGGACATG
TGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGAAGGCCAG
CTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGA
AGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGG
AGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATC
CAGGGAGGAGGACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCGAACA
GCAGGGGCAGAGCAGCCCTCCTTCGAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTTCTGGG
GCCAGCCCAACACCTGGCTTGGGCTCACTGTCCTGAGTTGCAGTAAAGCTATAACCTTGAA
TCACAA

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FIGURE 64

MTTWSLRRRPARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
 IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDGSGNLDLEAFVLMA
 AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQ
 YKRGGP I IAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKGLSKGI VQGVLAT
 INLQSTHELQLLTTFLFNVQGTQPKMVMYWTGWFDGSGGPHNILDSSEVLKTYSAIVDAGS
 SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDEFGSISGIP
 LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYEN
 TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
 IDDQRKGLIGNLYLNDSPKKNFRIYSLDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSLSIS
 STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
 LQFTETPHLGRNQYIK

Signal sequence: amino acids 1-27

Casein kinase II phosphorylation site: amino acids 141-118,
 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site: amino acids 146-152, 236-242, 240-246,
 244-250, 287-293, 309-315, 320-326, 366-372, 423-429, 425-431,
 441-447, 503-509, 580-586

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FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
 CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
 AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA
 GGCAGACACTCGGTTCGTTTCGTAGTGGATAGGGGTCATGACCGGTTTCTCCTAGACGGGGCCC
 CGTTCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACATA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCCTTTCTGA
 ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTTCAGGTGGAGAATGAATATGGTAGC
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG
 AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTCTATAACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAATCTTTACCCTGCTT
 CGGAAGTATGAACCCCATGGGCCATTGGTAACTCTGAGTACTACACAGGCTGGCTGGATTA
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
 AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT
 TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCCAT
 TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
 GAACCTATATGACCCATACCATTTTTTGAGCCAACACCATTTCTGGGTGCCAAATAATGGAGTC
 CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTTGGAGCGAAATATGAG
 AGACAAACTATTTTTGACGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
 GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
 GTGGTTTTCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
 ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
 ACAACAGACCCTCTACGTGCCAAGATTCCTGCTGTTTCCTAGGGGAGCCCTCAACAAAATTA
 CATTGCTGGAAGTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC
 CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCTTTTCAGCTGATACACTGAG
 TGCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
 CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA
 CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG
 ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
 AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
 GACACTCCATCTCAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TL LRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMFMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLEPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTIILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSGDFTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence: amino acids 1-27

N-glycosylation site: amino acids 97-101, 243-247, 276-280,
486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 4-8

Casein kinase II phosphorylation site: amino acids 148-152,
234-238, 327-331, 423-427, 469-473, 550-554, 603-607, 644-648

Tyrosine kinase phosphorylation site: amino acids 191-198

N-myristoylation site: amino acids 131-137, 176-182, 188-194,
203-209, 223-229, 227-233, 231-237, 274-280, 296-300, 307-313,
447-453, 484-490

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FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
 ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
 TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
 CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
 GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
 CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGAGATTG
 AAAAAGTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
 CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAGT
 AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
 TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
 TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
 CCTTCGAGAGTTGTACTTAATAGGCAATTTGAAGTCTGAAAACAATAAGATGATAGGACTTG
 AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCCTCACGTGAAGAGCAATTTGACCAAAGTT
 CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCATAATGACGGCAC
 TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAAGTCCAGA
 ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
 TAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT
 GACTTGTTTTAAATTTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
 AAAACTTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
 AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
 AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
 CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
 TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
 CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG
 TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
 AATATTCCTTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
 AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
 ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
 GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG
 AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTAAATTGTTTGTAACTTGGAT
 GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
 TTCTTACTAAAAA

APPROVED	O.R. FIG.	
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FIGURE 68

MAYMLKKLLISYISIIICVYGFI CLYTLFWLFR IPLKEYSFEK VREESSFS DIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISR NAQDKQELH LFM LSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELH LCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLSEN NKMIGLES LREL RHLKILHVKS NLT KVPSN
ITDVAPHLTKLVIHNDG TKLLVLNSLKKMMNVAE LELQNC ELERIPHAIFSL SNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPAVAVFSLQ
KLRC LDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLS QLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDH LFD TLPLEVKEALNQDINIP
FANGI

Signal sequence: amino acids 1-20

N-glycosylation site: amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 326-330

Casein kinase II phosphorylation site: amino acids 48-52,
133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site: amino acids 349-355,
375-381

N-myristoylation site: amino acids 78-84, 124-130, 212-218,
392-398

APPROVED	FIG. 69	
BY	CLASS	SUBCLASS
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FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCTTTTCATTGACAACTGAC
 TTTTTTTTATTTCTTTTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGA
 CATTTGTGTTTTACACACATAAGGATCTGTGTTTGGGGTTTCTTCTTCCCTCCCCTGACATTG
 GCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGGGCTCAGTGCTTGCTTGCACTTAT
 CTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTCATCGCTGGTG
 GTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCTGTCTCTGTCTTTACTTCAAATAACAC
 AACGCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAA
 GGTGTGGTGGGCCAAGAAGCCAGCCAGGCCAAAACCATTGCCACGGAGTCTTGTCTTGGCCTGG
 AGTGCTGTGAAGGATATAGAATGTGTGCCAGTTTGTATTCCCTGCCACCTTGCTGTTGCGAC
 ATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAAGCAGAGCCCTGAAGACTTCA
 ATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAGCTCCCCA
 TCAGTTTCATGGAAAATAACTCAGTGCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAG
 AGCTTCCACTGGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGG
 AATGCTGATAAACCAGTCACACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCT
 GGAAGTGACGTTTCCCTGGAGGTGTCCAGAAAGCTGATGTAACACAGAGCCTATAAAAGCTG
 TCGGTCCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTAAGAAGGCTCATGCCATT
 GACCTCTTAATTCTCTCTCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAATGCAA
 GCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAA
 CTCAATCCCAGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAAACAAAGCATCAGAAT
 TATCTTTTCTCTATGTCCAGCTTGATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCT
 TTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGGCAAGTCTGCAGTAAAAACGACTATGTT
 CCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACTGACTCAGCAAGAAT
 TCAAAGAAGTGTCTTTGTCTTCTACTACTTCTTCTCTCTAATCTCTATTCCAAAGTGTG
 GCGGTTACCTGGATACCTTGGAAGGATCCTTACCAGCCCCAATTACCCAAAGCCGCATCCT
 GAGCTGGCTTATTGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAACTT
 CAAAGAGATTTTCTAGAAATAGACAAACAGTGCAAATTTGATTTTCTTGCCATCTATGATG
 GCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGTGGCCGTGTGACTCCCACCTTCGAA
 TCGTCATCAAACCTCTCTGACTGTCTGTGTTGTCTACAGATTATGCCAATTCTTACCGGGGATT
 TTCTGCTTCTTACACCTCAATTTATGCAGAAACATCAACACTACATCTTTAACTTGCTCTT
 CTGACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAAT
 AACTTGCAACTAAAAGACCCAACCTTGACAGACCAAAATTATCAAATGTTGTGGAATTTTCTGT
 CCCTCTTAATGGATGTGGTACAATCAGAAAGGTAGAAGATCAGTCAATTACTTACACCAATA
 TAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACCCGTCAGAAACAACTCCAGATT
 ATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACAGAAGATGA
 TGTAATACAAAGTCAAAATGCACTGGGCAAAATATAACACCAGCATGGCTCTTTTGAATCCA
 ATTCATTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACTCTTTT
 GTTCAAGTTAGTCTGCACACCTCAGATCCAAATTTGGTGGTGTCTTCTTGATACCTGTAGAGC
 CTCTCCCACCTCTGACTTTGCATCTCCAACCTACGACCTAATCAAGAGTGGATGTAGTCGAG
 ATGAAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGATTCCAGTTTAATGCCTTT
 AAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTTGATATGTGATAGCAG
 TGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCAT
 ATAAATGGAAAACAGATTCCATCATAGGACCCATTCGTCTGAAAAGGGATCGAAGTGCAAGT
 GGCAATTCAGGATTTTCAAGCATGAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAG
 TGTGCATCTGTTTTCTTCATGGTTCTAGCTCTGAATGTGGTGACTGTAGCGACAATCACAG
 TGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTGCAGAAGTATTAAC
 ACAGGTCCAACCCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGTGG
 CTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAA
 AAA

APPROVED	FIG.	
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FIGURE 70

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
 ERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQGVCCKNDYVPVFESSSSTLT
 FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
 EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVLS
 TDYANSYRGFSASYTSIYAENINTTSLTSSDRMRVVISKSYLEAFNSNGNNLQKDPTCRP
 KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIVKCEMGNST
 VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
 LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
 QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDISIIGPIRLKRDRSASGNSGFQHETHA
 EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence: amino acids 1-24

Transmembrane domain: amino acids 571-586

N-glycosylation site: amino acids 29-33, 57-61, 67-71,
 148-152, 271-275, 370-374, 394-398, 419-423

Casein kinase II phosphorylation site: amino acids 22-26,
 108-112, 289-293, 348-352, 371-375, 379-383, 408-412, 463-467,
 520-524, 556-560

Tyrosine kinase phosphorylation site: amino acids 172-180,
 407-415, 407-416, 519-528

N-myristoylation site: amino acids 28-34, 38-44, 83-89,
 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGAC**ATG**CGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTG
TGCTGCCGCCGCCGCCGTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC
CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTGATCCACTG
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATAACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGAT
TTTGGAACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGG
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCGTGGAACCTGGAATGCCATAGATGAGGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGACTGTACTATTCCCTTTTTGA
ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGCCCTGGTT
ATATAATGAAAGCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACCTGCATGACAATAGACAAACTGTCCTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCCAAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCCCTTGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATC**TAA**AGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTTCCCCTA
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACCTTTGCCATTAAAGTC
TCTTCACATTGATTTGTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTTG TGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAACATAGAGAAG
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAA
GTTTTTCTTTCTTCAATTATAAATAAACATAAGTGTACTGTAACTTTACAAACGTTTTAATT
TTTAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAACATAAACTCATTGTGCAA
ATGTAA

APPROV	J.C. FIG.	
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FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence: amino acids 1-28

N-glycosylation site: amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site: amino acids 32-36,
182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site: amino acids 361-369,
389-397

N-myristoylation site: amino acids 143-149, 178-184, 255-261,
272-278, 428-434

Leucine zipper pattern: amino acids 410-432

Alpha-L-fucosidase putative active site: amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
 TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
 TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
 CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCT
 TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCCGAACCAGC
 AGCTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
 GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA
 TGGATTTCGTGGTTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
 TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
 ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA
 AACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
 ACTCTACAATACCTGCCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG
 AGAAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC
 TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
 CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC
 TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
 CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
 AACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA
 GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
 TTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT
 GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
 CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
 TTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAA
 GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
 TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGAC
 CCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA
 AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
 ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
 GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
 ATCACTGTTTGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
 AGGAAATATACTTTTACAAGTAACAAAAATAAAAACCTCTTATAAATTTCTATTTTTATCTGA
 GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAGTAATAAAATTCA
 ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
 TGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA
 GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTTTGTGCTGAGACTAATCTT
 ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG
 TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA
 GCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
 AGCATTTAGAAAACCTT

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FIGURE 74

MARCFSLVLLLTSIWTTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
 LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQF
 AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
 APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFF
 GAAAGLGFCYVKRYVKAFPFNTKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
 SKTTVRCLEAEV

Signal sequence: amino acids 1-16

Transmembrane domain: amino acids 235-254

N-glycosylation site: amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site: amino acids 145-149,
 214-218

Tyrosine kinase phosphorylation site: amino acids 79-88

N-myristoylation site: amino acids 23-29, 65-71, 234-240,
 235-239, 249-255, 253-259

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FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGG
 CTCGCCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA
 ACTGCCGCGGCTCTGCCACGGTCTGCCCACCAACGCGAAGACGGTAACCCGTGTGACTTTG
 ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
 TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
 TCTTTTCTTCCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTC
 TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
 ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
 TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
 GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
 AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
 GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
 AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
 AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
 TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT
 CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG
 CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
 GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACTGTTTCACTGGAGCAAGAAAGAGATC
 TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATC
 AGCTATTCAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAG
 TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA
 CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
 TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
 TTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
 TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC
 TAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT
 TCCTTTTG

APPROVED	D.G. FIG.	
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DRAFTSMAN		

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK.

Signal sequence: amino acids 1-48

Transmembrane domain: amino acids 111-125

N-glycosylation site: amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 154-158, 265-269

Casein kinase II phosphorylation site: amino acids 51-55,
145-149, 245-249, 286-290, 288-292

N-myristoylation site: amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1: amino acids
244-253

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FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
 GGGCCCCAGCCTGGCCCGGGTCACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA
 TTGCTCCTGCTGCCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
 CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
 TGGTGGAGACACCCGAGGAGACCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
 CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGAAGCT
 GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
 TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
 ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA
 GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA
 ACGGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
 GTGGCCTCCTTTGAGCAGCTCTTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
 CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCGGTGGCC
 CAGGCCTGGCACCTGGCGTGCGAAGCTACGGCCCCCGCCACCGCCGCCTGCACCGCTATGAT
 GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCCCTGAGAAGCT
 GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC
 AGCTCTTTGCCGCCTGGAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
 GGCAGCGTCCGCTACCCTGTGGTTACCCGCATCCTAACTGTGGGGCCCCAGAGCCTGGGGT
 CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC
 ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT
 CGTTTTCCCTTGTGGGTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
 TTAAACATTTTTTTTACTATTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG
 GATGCCCCACTCCAGGAATCATGCTTGCTCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG
 GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCCAGAGTGGGC
 GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCCCT
 CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC
 CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA
 GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCCCTCCCCGTTCCCCCT
 TCCCCCTCTCGGTTCCAAAGAATCTGTTTTGTGTGTCATTTGTTTCTCCTGTTTCCCTGTGTGG
 GGAGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGTATGACTGCCTTCCGCCAA
 AA
 AA
 AA

A

APPROVED	2.5. FIG.	
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DRAFTSMAN		

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FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
 GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDLVAIGLRHRSFGDYQGRVHLRQD
 KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
 VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
 HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
 CDAGWLADGSVRYPVVHPPHNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence: amino acids 1-17

Casein kinase II phosphorylation site: amino acids 29-33,
 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site: amino acids 137-145

N-myristoylation site: amino acids 36-42, 184-190, 208-214,
 237-243, 297-303, 307-313

APPROVED	O.G. FIG.	
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DRAFTSMAN		

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FIGURE 79

[illegible]

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 80

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
 EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
 YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD SMATRE
 ELTAFLHP EEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEP AWVQTERQQ
 FRDFRDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
 GSQATNYGEDLTRHHDEL

Signal sequence: amino acids 1-20

N-glycosylation site: amino acids 140-144

Casein kinase II phosphorylation site: amino acids 72-76,
 98-102, 127-131, 184-188, 208-212, 289-293, 291-295, 298-302

N-myristoylation site: amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence: amino acids 325-330

APPROVED	E.C. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
 GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCTCTGTCCCTGTTTCTTTGTCGCTCCCAG
 CCTGTCTGTCTGTCGTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTGCACACCGATCCTG
 GGCTTCGCTCGATTTGCCGCCGAGGCGCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
 CGGGTCTGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCAGGGGCTCT
 GAGGAGGTGACGCGCGGGGCTCCCGCACCTTGGCCTTGCCCGCATTCTCCCTCTCTCCCAG
 GTGTGAGCAGCCTATCAGTCACCAATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG
 TGTCTGCTGCTGCTGCCGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
 TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC
 CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC
 TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
 GGTCTGCTTCTTTACAGTAACTAAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
 GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG
 CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
 CCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
 GAAGGACCACATGTGGGCCTTGTTCAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA
 AAACCTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
 ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA
 GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
 AGCCTATCCCTGAAGAACTGGGGATGGTTTCAAGATGTCACATTTGTTGACAAGGCTGTCTGT
 CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAATACGTAAA
 GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
 CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTTGGAGATAGCAATTTCCGCCCTC
 ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT
 AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA
 AAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
 GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA
 CTTCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
 CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
 AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTCACAGGATT
 AGAACCAATTGTTTCTGATGTCATCAGAGGCATTTGTAGAGATTTCTTAGAATCCCAGCAAT
AATGGTAACATTTTGACAACCTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT
 CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGTATGTCAAC
 AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
 GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
 TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

APPROVED	D.C. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEF SVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVT FVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNI AFLI
DGSSSVGDSNFRLMLEFVSNI AKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAF FTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence: amino acids 1-24

N-glycosylation site: amino acids 100-104, 221-225

Casein kinase II phosphorylation site: amino acids 102-106,
129-133, 224-228, 316-320, 377-381, 420-424, 425-429, 478-482,
528-532

N-myristoylation site: amino acids 10-16, 23-29, 81-87,
135-141, 158-164, 205-211, 239-245, 240-246, 261-267, 403-409,
442-448, 443-449

Amidation site: amino acids 145-149

APPROVED	D.E. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCCGGCCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT
GCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTACA
TCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACCAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTG
TGCTTTCAGCTGTTGCAGATGAAATGTTCTGTTTACCCTGCATTACATGTGTTTATTCATCC
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

APPROVED	D.C. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 84

MQR LGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSY PQEEATLNEMFREVEELMEDTQ
 HKLRS AVEEMEAEEAAAKASSEVNLANLP SYHNETNTDTKVG NNTI HVHREIHKITNNQTG
 QMVFSETVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCR GQRM LCTR DSECCG
 DQLCVWGHCTKMATRGSNGTICDNQRDCQ PGLCCAFQ RGLLFPVCTPLPVEGELCHDPA SRL
 LDLITWELEPDGALDRCP CASGLLCQPHSHSLVYVCKPTFVGS RDQDGEILLPREVPDEYEV
 GSFMEEV RQELEDLERSL TEEMALGE PAAAAAALLG GEEI

Signal sequence: amino acids 1-19

N-glycosylation site: amino acids 96-100, 106-110, 121-125,
204-208

Casein kinase II phosphorylation site: amino acids 46-50,
67-71, 98-102, 135-139, 206-210, 312-316, 327-331

N-myristoylation site: amino acids 202-208, 217-223

Amidation site: amino acids 140-144

APPROVED	FIG.	
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FIGURE 85A

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCT
CAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAACACA
CATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAAGACTCA
CAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGACAGGCCTGG
CCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGGGCCAGGCACGG
TGA CTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAG
GAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATT
AGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATC
GCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCGCTGCACTCCAGCCTGGGT
GACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGAGGGGTAGATACTGCTTCTCT
GCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGCCCCCTGATGGGGCCTGGCAATGA
CTGAGCAGGCCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
CGCCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTTCCCTTGGGCCCTGGCAGGGTTGCTGAC
CCTTACCCTGCAAAACACAAAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCC
TGCAGCTCCACCATGAGGCTTCTCGTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCAC
TGCCACTGTGCCCCGTGGTACCCTGGCATGTTCCCTGCCCCCCTCAGTGTGCCTGCCAGATCC
GGCCCTGGTATACGCCCCGCTCGTCTTACCGCGAGGCTACCACTGTGGACTGCAATGACCTA
TTCTTGACGGCAGTCCCCCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAA
CAGCATTGTCCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACC
TGTCCCAGAACAGCTTTTTCGGATGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTG
AGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGC
CAGCCTACAGGA ACTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCAGGGCCTTTT
CTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGC
CGCTGGTTTGAAATGCTGCCCAACTTGAGATACTCATGATTGGCGGCAACAAGGTAGATGC
CATCCTGGACATGAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGA
ACCTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
TATGACAACCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTT
CCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGC
ACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTG
GTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA
CCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCA

To Figure 85B

APPROVED	FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 85B

From Figure 85A

GTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCACGGC
AACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGTCCGCTT
CATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCCGGTCCGTG
AGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCTCATCTCCCCACGAAGCTTCCCC
CCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGCACTGGCCGAACC
CGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCA
GGAGGTACCGGGTGTACCCCGAGGGGACCCTGGAGCTGCGGAGGGTGACAGCAGAAGAGGCA
GGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGGCTGACACTAAGACGGTTAGTGTGGT
TGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCGGGTGC
AGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTCACCCACCCAACACAGTGTCCACC
AACCTCACCTGGTCCAGTGCCCTCCTCCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCCT
GCCTCGGGGAACCCACAGCTACAACATTACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCT
GCCTGCAAGTGGCCTTTGCTGATGCCACACCCAGTTGGCTTGTGTATGGGCCAGGACCAA
GAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCCTGGGCTCATTGCCATCCTGGCTCT
CGCTGTCCTTCTCCTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAAGG
GTGTGGGTGGGAGGCGCCTCTCCCTCCAGCCTGGGCTTCTGCGGCTGGAGTGCCCTTCT
GTCCGGGTTGTGTCTGCTCCCCCTCGTCCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATC
CTCAGAAGGGGAGACACTGTTGCCACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTC
AGCAGTAGAGAAATCACTAGGACTACTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCC
CTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGG
GGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTC
ACCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCC
TGCTCCCCATCTTCTCTCTGCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGT
GTCCCCGGGCTGCACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGT
GCCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGT
GGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCATC
TCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGG
AGAAATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAA
TAAATAATAACAATAAAAAA

APPROVED	FIG. FIG.	
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FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
 VPPALPAGTQTLILLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
 EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
 MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNO
 LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKFAVNLP
 ELTKLDITNNPRLSFIHPRAFHHLPMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
 CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPPFREMTDHCLPLISPRSFPPSLQ
 VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAEEAGLYT
 CVAQNLVGADTKTVSVVVGRRALLQPRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
 SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
 CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVV
 SAPLVLPWNPGRKLPRSSSEGETLLPPLSQNS

Signal sequence: amino acids 1-18

Transmembrane domain: amino acids 629-648

N-glycosylation site: amino acids 94-98, 381-385, 555-559,
583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 485-489

Casein kinase II phosphorylation site: amino acids 46-50,
51-55, 96-100, 104-108, 130-134, 142-146, 243-247, 313-317,
488-492, 700-704

Tyrosine kinase phosphorylation site: amino acids 532-540

N-myristoylation site: amino acids 15-21, 493-499, 566-572

Amidation site: amino acids 470-474, 660-664, 692-696

APPROVED	N.C. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 87A

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACA
 TTGTGTACCGCCTCTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATC
 TGCTACACCGTCTACTACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGA
 GAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCACCCCCTGGCCACACTCTTCAAGATCC
 TGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTGG
 TGGATGCTACGGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTA
 CAGCGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACG
 ACCCGCTCTACTCCAAGCGCTTCGCCGTCTTCCTGTCGGAGGTGAGTGAGAACAAGCTGCGG
 CAGCTGAACCTCAACAACGAGTGGACGCTGGACAAGCTCCGGCAGCGGCTCACCAAGAACGC
 GCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCATCCCTGACACTGTGTTTGACC
 TGGTGGAGCTGGAGGTCCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCCCAGCATT
 GCCCAGCTCACGGGCCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCC
 TGCCTGGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGG
 AGATCCCGCTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTG
 AGCGCGGAGAACAACCGCTACATCGTCATCGACGGGCTGCGGGAGCTCAAACGCCTCAAGGT
 GCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCACAGATGTGGGCGTGCACC
 TGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCCTAACAGCCTCAAGAAG
 ATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCAT
 CTTACGCCCTCCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGG
 AGATCATCAGCTTCCAGCACCTGCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATC
 GCCTACATCCCCATCCAGATCGGCAACCTCACCAACCTGGAGCGCCTCTACCTGAACCGCAA
 CAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCGCTACCTGGACCTCA
 GCCACAACAACCTGACCTTCCTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCTA
 GCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCG
 GGCCCTGCACCTGGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCA
 ACCTGACGCAGATCGAGCTGCGGGGCAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAG
 TGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGAGGACCTGTTCAACACACTGCCACC
 CGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAGGCCGGCCCAGC
 ACAGCAAGCAGCAGGACCGCTGCCAGTCCTCAGGCCCGGAGGGGCAGGCCTAGCTTCTCCC
 AGAACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCAGGAGCCTGGGGCCGCTTGTGAGT
 CAGGCCAGAGCGAGAGGACAGTATCTGTGGGGCTGGCCCCTTTTCTCCCTCTGAGACTCAGC

_____ To Figure 87B

APPROVED	FIG. 87B	
57	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 87B

From Figure 87A

TCCCCCAGGGCAAGTGCTTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATAATCA
GGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCCTGGGA
CCCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCACCTCCTTCATCCAGATAACT
TATACATTCCCAAGAAAGTTTACAGCCAGATGGAAGGTGTTTACAGGAAAGGTGGGCTGCCTTT
TCCCCTTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTGAGCAGAG
TGGTCCGGGGCGAACCAGCCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTG
CGGTCCACGGGAGAGCAGGCCTCCAGCTGGAAAGGCCAGGCCTGGAGCTTGCCTCTTCAGTT
TTTGTGGCAGTTTTAGTTTTTTGTTTTTTTTTTTTTAATCAAAAAACAATTTTTTTTAAAA
AAAAGCTTTGAÂAATGGATGGTTTGGGTATTAAAAAGAAAAAAAAAACTTAAAAAAAAAAAAAG
ACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAG
CCAGACGTTGAACTGTGTTTCCCTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGG
TGTGACCTTGGTCCAGGAGTTCTATTTGTTCTTGGGAGGGAGGTTTTTTTGTGTTGTTTTT
GGGTTTTTTTGGTGTCTTGTGTTTCTTTCTCCTCCATGTGTCTTGGCAGGCACTCATTTCTGT
GGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAGACTCGGGTTGGCTAA
TCCCCGGATGAACGGTGCTCCATTTCGCACCTCCCCTCCTCGTGCCCTGCCCTGCCTCTCCACG
CACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTTCCCCACCTCCTGCGG
CATGGGTGTGTCCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGG
TCCTTCATGAAGAGCAGACACTTAGAGGCTGGTTCGGGAATGGGGAGGTCGCCCCCTGGGAGGG
CAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGCCTGGAGTGCACACAGCCCAGTCGGC
ACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTTAGAAGGGTCCCC
GCCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATG
TCCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCGTGTCATTGGATATAATCCTCAGAA
ATAATGCACACTAGCCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACTT
GTAGACTCGGTCACAGTATCAAATAAAATCTATAACAGAAAAAAAAAAAAAAAAA

ROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
TSMAH		

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FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFO
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain: amino acids 51-75 (type II)

N-glycosylation site: amino acids 262-266, 290-294, 328-332,
396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 85-89

Casein kinase II phosphorylation site: amino acids 91-95,
97-101, 177-181, 253-257, 330-334, 364-368, 398-402, 493-497

N-myristoylation site: amino acids 173-179, 261-267, 395-401,
441-447

APPROVED	E.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
 CCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
 GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
 TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGATCAT
 GTGGCTTCAGGGCGGTCCAGGCGGTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC
 CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
 GTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
 CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
 AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
 ATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
 TGCCTTGGGTGATTCTTGGATCTCCCCGTGTTGATTCGGTGCTCTCCTGGGGACCTTACCTGT
 ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
 CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
 GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCCCA
 CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTTCAGCGC
 CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
 GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
 TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTTGTGGACGAGTTGCTGGAGGCAGGGATC
 AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTG
 GGTGCGGAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
 ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC
 TACTGGATTCTGAAAGCTGGTCATATGGTTCCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
 GATGAGACTGGTGAATCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
 TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
 AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
 GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
 TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

APPROVED	H. O. FIG.	
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FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKATQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLORDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMAKMMRLVTQQE

Signal sequence: amino acids 1-25

N-glycosylation site: amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 101-105

Casein kinase II phosphorylation site: amino acids 204-208,
220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site: amino acids 22-28, 76-82, 79-85,
80-86, 119-125, 169-175, 187-193, 195-201, 331-337, 332-338,
360-366

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FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
T TACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTGTTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

APPROVED	O.G. FIG.	
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FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLW
DSHVCVSVLLSHRWALTAAHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNK
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLEFELLWALPL
LGPV

Signal sequence: amino acids 1-18

N-glycosylation site: amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site: amino acids 86-90,
134-138, 161-165, 190-194, 291-295

N-myristoylation site: amino acids 2-8, 44-50, 101-107,
225-231, 229-235, 239-245, 259-265, 269-275

Amidation site: amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site: amino
acids 252-263,

Serine proteases, trypsin family, histidine active site:
amino acids 78-84

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FIGURE 93

CCCACGCGTCCGCGGACGCGTGCGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
 CTTTGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC
 TGCCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
 GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCCGATCCCAG
 CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
 CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCT
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
 TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
 ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
 TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
 GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACAACTTGACCTCACAAGACGTGG
 GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTTGAGCAGTATTTCCATGAC
 TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
 CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGATTGAGGCCAGTCTAGATGTGCAGT
 ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
 GGACAGGAGCCCTTCTGAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
 AACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGT
 GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
 CCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACAAATGAAA
 TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
 GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
 CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGGTGGTCAGCAACA
 GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA
 TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCT
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC
 TGGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCTTTCCTATC
 AGGAGAGATGGCTTGTCCTTGCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTG
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCTGAAA
 TGCTGTGAGCTTGACTTGACTCCCAACCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
 CCTGCCTTAGATTCTCAATAAGATGCTGTAAGTAGCATTTTTTGAATGCCTCTCCCTCCGC
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGACTA
 TTTCACTTGATATTCATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTTACTCT
 TTCTTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG
 GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAAGTTCTCTG
 ACTACTCTTGCTCTCCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC
 TCCATTTGTAGATTTTTGCTCTTCTCAGTTTACTCATTGTCCCCTGGAACAAATCACTGACA
 TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
 TGTAACAAA

APPROVED	O.C. FIG.	
LY	CLASS	SUBCLASS
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FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQONVERLS
 ELVQAVSDPSSPQYGKYLTLNVADLVRPSPLTLHTVQKWLLAAGAQQKCHSVITQDFLTCWL
 SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
 EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
 GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
 LSNESALPHVHTVSYGDDSDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
 QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
 HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPVVSGTSASTPVFGGILSLINEHRILSG
 RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence: amino acids 1-16

N-glycosylation site: amino acids 210-214, 222-226, 286-290,
 313-317, 443-447

Glycosaminoglycan attachment site: amino acids 361-365,
 408-412, 538-542

Casein kinase II phosphorylation site: amino acids 212-216,
 324-328, 392-396, 420-424, 525-529

N-myristoylation site: amino acids 2-8, 107-113, 195-201,
 199-205, 217-223, 219-225, 248-254, 270-276, 284-290, 409-415,
 410-416, 473-479, 482-488, 521-527, 533-539, 549-555

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FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKPKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDELYQQCD
AQPASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence: amino acids 1-19

N-glycosylation site: amino acids 93-97, 207-211

Glycosaminoglycan attachment site: amino acids 109-113,
316-320

Casein kinase II phosphorylation site: amino acids 77-81,
95-99, 108-112, 280-284, 351-355

N-myristoylation site: amino acids 159-165, 162-168, 202-208,
205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site:
amino acids 171-177

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FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGGCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCGCGGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCCAC
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT
CTCCAAAAAAAAA

APPROVED	G.G. FIG.	
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FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVP IIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence: amino acids 1-32

N-glycosylation site: amino acids 62-66, 96-100, 214-218,
382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931,
939-943, 956-960

Glycosaminoglycan attachment site: amino acids 826-830

Casein kinase II phosphorylation site: amino acids 17-21,
39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327,
347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743,
783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017,
1019-1023, 1021-1025

Tyrosine kinase phosphorylation site: amino acids 607-615

N-myristoylation site: amino acids 179-185, 197-203, 320-326,
367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

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FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAATCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATAACCACTCAAAGGG
TGAAGAGGTGAGCTGTCTCCTGTCTATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC
GGGCCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

APPROVED	U.S. FIG.	
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FIGURE 100

MHGSCSFMLLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE
 LAFAKAYARQCVWGHNKERRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
 MCGHYTQVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPHYQEGTPCSQC
 PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFVLVTEV
 SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
 THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLAS
 VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGDPKPSV
 SGLNSGPGHVWGPLLGLLLLLPPLVLGIF

Signal sequence: amino acids 1-22

N-glycosylation site: amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site: amino acids 439-443

Casein kinase II phosphorylation site: amino acids 29-33,
 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site: amino acids 123-129, 143-149, 152-158,
 169-175, 180-186, 231-237, 250-256

Amidation site: amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature: amino acids
 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:
 amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:
 amino acids 160-172

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FIGURE 101A

GTAAGTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAG
 TTATGGTGGACGTACTTCTGTTGTTCTCCCTCTGCTTGCTTTTTTCACATTAGCAGACCGGAC
 TTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTTCG
 AGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCGGCAA
 ATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAA
 GAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAAGTGC
 ATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAAC
 CTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATC
 TCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTCGAATTGAACCGAAA
 CAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCTCTGAAAA
 TGCAAAGAAATGGAGTAACGAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAA
 ATTTTGAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCT
 GATGCTGCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGG
 AGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGAT
 TCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATTGGGAACAACAGAGTCAGCTA
 CATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAACAATG
 AAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGA
 CTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGC
 ATTGGAGCATCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAC
 AAATGAAGAACTGCAACAATTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTA
 AAATGGCTCCACAGTGGGTGGCGGAAACAACCTTTTCAGAGCTTTGTAAATGCCAGTTGTGC
 CCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTG
 ATGATTTTCCCAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTC
 AATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGGCTTGGA
 AAAAGACAATGAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAG
 GTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAG
 GGGAAATATCAGTGTGTCATCTCAATCACTTTGGTTTATCCTACTCTGTCAAAGCCAAGCT
 TACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGG
 CCATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAG
 GATGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGA
 CGTGTTCCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGA

Figure 101B

APPROVED	C.G. FIG.	
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FIGURE 101B

From Figure 101A

ACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCCCTAGAAACACCATCATTTTTTG
CGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCTGG
AGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGA
GGCACTTTTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCT
GGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAG
TGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACG
GATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGTGGTGGGCACGTCACCTC
GTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACCAACAC
AGATGAGACCAACTTGCCAGCAGATATTCTAGTTATTTGTCATCTCAGGGAACGTTAGCTG
ACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACCAGTTTGTACATCTTCA
GGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAG
TGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCCTTTGTCCGTTTTTGGGATCCACAGGCC
CTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACATATCATACAGGTTGC
AGTCCTGACCCAAGAACAGTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAGGA
GTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGT
GGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATG
AAAAATCTGTGTCTAAACAAGTCCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGT
TGCCTCGAGTAATTCTTTCATGGGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATG
CCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCAT
TCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGA
AGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGT
CTTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAG
TGAACTTTTATTTAAAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAA
GGATAAAAATGCTTTATTTATACAGATGAACCAAAATTACAAAAGTTATGAAAATTTTTAT
ACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTTAACTTTGTTTTATGCA
AAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGC
CAGATTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACA
TTTTTTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATT
TGAA

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FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSEKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHL SRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWL PQWVAENN FQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTD FPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPLVVTER
HFFAAGNQLLIIVDSVDSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNL PADIPSYLSSQGTLD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGS DPFETYHTGCS PDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEEHNHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence: amino acids 1-19

Transmembrane domain: amino acids 746-765

N-glycosylation site: amino acids 62-66, 96-100, 214-220,
382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931,
939-943, 956-960

Glycosaminoglycan attachment site: amino acids 826-830

Casein kinase II phosphorylation site: amino acids 17-21,
39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327,
347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743,
783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017,
1019-1023, 1021-1025

Tyrosine kinase phosphorylation site: amino acids 607-615

N-myristoylation site: amino acids 179-185, 197-203, 320-326,
367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTG
 CCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAAC
 TGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGAGCCCTGGATCTTAACACAA
 ATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGACCCGCGGG
 GGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCCCCACCCCAA
 AAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGTATGTTTATTTTT
 CTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTT
 AGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCCACAAGAGGAG
 AGGAAATTAATAATACATCTGCAAAGAAATTCAGAGAAGAAAAGTTGACCGCGGCAGATTG
 AGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGATTTGTGCCTATGTTGACTAA
 AATTGACGGATAAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTTTAAATTTTTATT
 CCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTTAACCACCTGGATTTCCATCTGGAT
 GTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCCAGAAGGACCAACACCAGATAAAT
 TATGAATGTTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAC
 AGGGCCCTATTTGACCCCTGCTTGTGGTGTGCTGGCTCTTCAACTTCTGTGGTGGCTGG
 TCTGGTGC GGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGA
 TTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTGCTG
 AACCTCCATGAGAACC AAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTT
 GGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTC
 TGGCGAACCTCAACACTCTGGAACCTTTTGACAATCGTCTTACTACCATCCC GAATGGAGCT
 TTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTTGCGAAACAACCCCATTGAAAGCATCCC
 TTCTTATGCTTTTAAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGAC
 TTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGGTATTTGAACCTTGCC
 ATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCT
 TTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGATGCACCTTCAA
 AACTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAG
 TCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCAC
 TCCCTTGCATCATCTAGAGCGGATACATTTACATCACAACCCTTGGAACCTGTAACGTGACA
 TACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTTGTGCCCCG
 TGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAG
 CTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGA
 ACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAA
 TTTACAAATGTAACGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAATCCGTTG
 GGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTAC
 TTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATA
 CAATGTGGGTCCCCTCCAGTGGTCTGACTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTGACAGAGAAAACCTTCACCATCCCAGTGACTGATATAAACAGTGGG
 ATCCCAGGAATTGATGAGGTCATGAAGACTACCAAATCATCATTGGGTGTTTTGTGGCCAT
 CACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGC
 AAAACCATCACGCCCCAACAAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGA
 GACACACCCATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTA
 TAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTC AATACACA
 GTTCAGTGCATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAA
 ATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAA
 ATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAAAA
 AAGAAAAGAAATTTATTTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAA

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FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSCSCSNQFSKVIC
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHNPWNCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDGTGMYTCMVNSVGN
TTASATLNVTAATTTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNTVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence: amino acids 1-44

Transmembrane domain: amino acids 523-543

N-glycosylation site: amino acids 278-282, 364-368, 390-394,
412-416, 415-419, 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 183-187

Casein kinase II phosphorylation site: amino acids 268-272,
417-421, 465-469, 579-583, 620-624

N-myristoylation site: amino acids 40-46, 73-79, 118-124,
191-197, 228-234, 237-243, 391-397, 422-428, 433-439, 531-537

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FIGURE 105A

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTG
 CTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCG
 CGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGACCCCTCGGCTGGAAGTTTGTGC
 CGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGGACCGCGAT
GAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGCGCGGTGCTGG
 GCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCC
 GCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAA
 GCGGCTAGCGCGTCTTCCCAGGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACA
 ACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAA
 CTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCGGCAAATATTACACT
 TCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAGTTTCAGT
 CCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAAACTGCATTTCCAGCC
 CTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTT
 TGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCC
 CACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAA
 AATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCTCTGAAAATGCAAAGAAA
 TGGAGTAACGAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAAATTTTGCAGC
 TGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAG
 GAACTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCA
 GAAGCTCAGTGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCC
 TTGGCCTAAGCTTACTAAATACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGAT
 TGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTG
 GACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCC
 AAGGAAATCGGATCCGTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCAT
 CTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAA
 ACTGCAACAATTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCC
 CACAGTGGGTGGCGGAAAACAACCTTTAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAG
 CTGCTAAAAGGAAGAAGCATTTTTGCTGTTAGCCAGATGGCTTTGTGTGTGATGATTTTCC
 CAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTT
 TCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAGACAAT
 GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGT

_____ To Figure 105B

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FIGURE 105B

From Figure 105A

GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATC
AGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTAGAGTAAAT
ATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCAGC
CTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCA
CAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCCGAGGATGACGTGTTCTTT
ATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGG
AAGTATTTTACGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATTTTTTGGCGCCACTGT
TGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCTGGAGGAAGCCCT
CCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCACTTTTT
TGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACA
CATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCC
ACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCAC
TGTGGGTGTCGTGATCATAGCCGTGGTTTGTCTGTGTGGTGGGCACGTCACCTCGTGTGGGTG
TCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACCAACACAGATGAGACC
AACTTGCCAGCAGATATTCCTAGTTATTTGTCATCTCAGGGAACGTTAGCTGACAGGCAGGA
TGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACCAGTTTGTACATCTTCAGGTGCTGGAT
TTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGAT
GTGGAAGCTGCCACAGATCTGTTCCCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTT
GAAGGGAAATGTGTATGGCTCAGATCCTTTTGAACATATCATACAGGTTGCAGTCCTGACC
CAAGAACAGTTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCA
TGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACA
TGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGT
GTCTAAACAAGTCCTCTTTAGATTTTGTGCAATCCAGAGCCAGCGTCGGTTGCCTCGAGT
AATTCTTTTCATGGGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAG
CTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAG
ACTTGGA CTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCAC
ATTTGTACCTTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTT
GGACACA TAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTA
TTTAAAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAT
GCTTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTTATACTGGGAATG
ATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTATC
TTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTTATAATGCCAGATTTCTT
TTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTAACATTTTTTTAAAT
AGAAGTTACTTCATTATATTTTGCACATTATTTTAAATAAAATGTGTCAATTTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLOHLELN RNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDSL DNAIMSLQGNAFSQMK
KLQQHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDE
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAH LRAQGGE
VMEYTTILRLREVEFEASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGH PAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLIIVDSVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
TVGVVIIAVCCVVGTSLVWVVI IYHTRRRNEDCSITNTDETNPADIPSYLSSQGT LADRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQH DSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKG NVYGSDPFETYHTGCSPDPRTV LMDHYEPSYIKKKECYPCHPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYD
LDT

Signal sequence: amino acids 1-27

Transmembrane domain: amino acids 808-828

N-glycosylation site: amino acids 122-126, 156-160, 274-278,
442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991,
999-1003, 1016-1020

Glycosaminoglycan attachment site: amino acids 886-890

Casein kinase II phosphorylation site: amino acids 99-103,
180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411,
524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847,
863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083,
1081-1085

Tyrosine kinase phosphorylation site: amino acids 667-675

N-myristoylation site: amino acids 14-20, 36-42, 239-245,
257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687,
774-780, 933-939

Leucine zipper pattern: amino acids 58-80, 65-87

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FIGURE 107A

CAAAACTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGA
 GCGCAGCTGAGACTGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAG
 CAGGGAAGGGGAAGCTGTGGTCTGCCCTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGA
 GCCCCTGGGTGGTCCCGTCCCCTATCCCTCCTTTATATAGAAACCTTCCACACTGGGAAGGC
 AGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGCTGATCTGCAGGCGCACAGCA
 TTCCGAGTTTACAGATTTTACAGATACCAAATGGGAAGGCGAGGAGGCAGAACAGCCTGCCT
 GGTTCATCAGCCCTGGCGCCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCC
 CAGAGCCGGGTGCTGCTGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCT
 TGCCGTGAGGGCCCCAGGATTTGGCCGAAGTGGCGGCCACAGCCTGAGCCCCGAAGAGAACG
 AATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGGAGCCCGGGCCTGGCCCAGCC
 GCGGTCAGCTGCCCCCGAGACTGTGCCTGTTCCCAGGAGGGCGTCGTGGACTGTGGCGGTAT
 TGACCTGCGTGAGTTCCCGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACA
 ACCAGCTGGAAAAGATCTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAAC
 CTGCAAAACAACCGCCTGACTTCCCGAGGGCTCCCAGAGAAGGCGTTTGAGCATCTGACCAA
 CCTCAATTACCTGTACTTGGCCAATAACAAGCTGACCTTGGCACCCCGCTTCTGCCAAACG
 CCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCTATGGGCTCACCTTTGGC
 CAGAAGCCAAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGCTGCC
 GGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCCTCATCCTGTCCAGCAACTTCCTGC
 GCCACGTGCCCAAGCACCTGCCGCCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTG
 GAGAAGATCCCCCGGGGGCCTTCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAA
 CAACTACCTGACTGACGAGGGCCTGGACAACGAGACCTTCTGGAAGCTCTCCAGCCTGGAGT
 ACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGCCGCGCAGCCTGGTG
 CTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCCG
 CAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGG
 CCTTCCAGGGCCTCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTG
 CCCAGTGGCCTGCCTCGCCGCGTGCACACCTCATGATCCTGCACAACCAGATCACAGGCAT
 TGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGGAGCTCAACCTCAGCTACAACCGCA
 TCACCAGCCCACAGGTGCACCGCGACGCCTTCCGCAAGCTGCGCCTGCTGCGCTCGCTGGAC
 CTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAA
 GGTCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGGCGCTGGCGGGCATGGCTCAGCTGC
 GTGAGCTGTACCTCACCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTG

_____ To Figure 107B

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FIGURE 107B

From Figure 107A

GACCTCGCCCATCTGCAGCTGCTGGACATCGCCGGGAATCAGCTCACAGAGATCGCCGGAGGG
GCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACACAAGATTAGTGCGGTGCCCGCCA
ATGCCTTCGACTCCACGCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGCTGGCTGTG
GGCTCCGTGGTGGACAGTGCCCTCCGGAGGCTGAAGCACCTGCAGGTCTTGACATTGAAGG
CAACTTAGAGTTTGGTGACATTTCCAAGGACCGTGCCGCTTGGGGAAGGAAAAGGAGGAGG
AGGAAGAGGAGGAGGAGGAGGAAGAGGAAACAAGATTAGTGACAAGGTGATGCAGATGTGACC
TAGGATGATGGACCGCCGGACTCTTTTCTGCAGCACACGCCTGTGTGCTGTGAGCCCCCAC
TCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCATCCACATGACACGGGCT
GACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGCACACA
CATCACACCCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCCAAACCACCACAGTCTC
TGTCACACCCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTGC
CCTGGCACACACAGGCACCCATTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACA
CCACACACACACATGCACAAGTCATGTGCGAACAGCCCTCCAAAGCCTATGCCACAGACA
GCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCTGTCCATCTGTCCGTC
CGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCTGG
AACTCACAAAAGCTGGCTTTTATTCTTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTG
CTGGCCTGGCCTGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCC
TCCCTGCCACGCCCTGGCAGGACACAGGCACTTTTCCAATGGGCAAGCCCAGTGGAGGCAGG
ATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGGCAGGAGTGAAGCAGAGGTGATGGGG
CTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTTGTTCTTCAGGCC
TGTGGGGGAAGTTCCGGGTGCCTTTATTTTTTATTCTTTTCTAAGGAAAAAATGATAAAAA
TCTCAAAGCTGATTTTTCTTGTTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGC
AAAAA

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FIGURE 108

MEGEEAEQPAWFHQPWPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSP EENEF AEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFPGDEP
EHTNHLSQLNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKA FEHLTNLNYLYIANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence: amino acids 1-48

N-glycosylation site: amino acids 243-247, 310-314, 328-332, .
439-443

Casein kinase II phosphorylation site: amino acids 68-72,
84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site: amino acids 19-25, 107-113, 213-219,
217-223, 236-242, 335-341, 477-483, 498-502, 539-545, 548-554

Leucine zipper pattern: amino acids 116-138, 251-273,
258-280, 322-344, 464-486, 471-493, 535-557

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FIGURE 109A

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCCT
CCGGGAGCGGCAGCAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAGAGGG
GCGCCTCCCATCGGCGCCCAACACCCCAACCTGTTCTCGCGCGCCACTGCGCTGCGGCCCA
GGACCCGCTGCCCAACATGGATTTTCTCCTGGCGCTGGTGCTGGTATCCTCGCTCTACTGC
AGGCGGCCCGCCGAGTTCGACGGGAGGTGGCCCAGGCAAATAGTGTCATCGATTGGCCTATGT
CGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTC
GCCTGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTC
ATCCTGGTTATGCTGGAAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGG
CCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTGCTACTGTCTCAACGGATA
TATGCTCATGCCGGATGGTTCTGCTCAAGTGCCCTGACCTGCTCCATGGCAAACCTGTCAGT
ATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCTGCACCTG
GCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCC
TAGATTTAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCATAAAGGCTTCG
ATCTCATGTATATTGGAGGCAAATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAG
TATCAGTGACAGCAGCTTTGCTCGATGTTATAACGTACGTGGGTCTACAAGTGCAAATGTAA
AGAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCCAAAGTTATGATTGAACCTT
CAGGTCCAATTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAATAAT
AATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTAT
CATTACCAACAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTC
CTACTCCACCACCACCACCACCCCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACC
CCAGAAAGGCCAACCACCGGACTGACAACTATAGCACCAGCTGCCAGTACACCTCCAGGAGG
GATTACAGTTGACAACAGGGTACAGACAGACCCTCAGAAACCCAGAGGAGATGTGTTCAAGT
TTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAAT
GACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGCGGCAGC
CAAAGCCCCAGGGGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCCTCATGCATTCAG
GGGACCTGTGCCTGTCATTCAGGCACAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTG
TTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTGGGGAAGAAATGGTGGCCATGGCTG
GAGGCAAACACAGATCACCTTGCGAGGGGCTGACATCAAGAGCGAATCACAAAGATTGATTAA
AGGGTTGGAAAAAAGATCTATGATGGAAAATTAAAGGAACCTGGGATTATTGAGCCTGGAGA
AGAGAAGACTGAGGGGCAAACCATTTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAG

_____ To Figure 109B

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FIGURE 109B

From Figure 109A

GGTGGCGACCAGCTGTTCTCCATATGCACTAAGAATAGAACAAGAGGAAACTGGCTTAGACT
AGAGTATAAGGGAGCATTCTTGGCAGGGGCCATTGTTAGAATACTTCATAAAAAAAGAAGT
GTGAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGATAAAAATTTGTCTATTTAAGA
TGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAAAGATGTTT
TGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAAT
TTAGGCATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCACCAAAT
GCTGAGCTCACTGAAATATCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAA
ACTATTTATTCCAAATGAGAGTATGATGGACAGATATTTTAGTATCTCAGTAATGTCCTAGT
GTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCCTTTCATTTGTTCAATGGA
TGATGTTTCAGATTTTTTTTTTTTTTAAGAGATCCTTCAAGGAACACAGTTCAGAGAGATTTT
CATCGGGTGCAATTCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGC
CCTGCCCCACACCGGCAGACCTTTCCTTCACCTCATCAGTATGATTCAGTTTCTCTTATCAA
TTGGACTCTCCCAGGTTCACAGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGT
CTTCTGTCATTTAACCTGGTAAAGGCAGGGCTGGAGGGGGGAAATAAATCATTAAGCCTTTG
AGTAACGGCAGAATATATGGCTGTAGATCCATTTTTAATGGTTCATTTCTTTTATGGTCATA
TAACTGCACAGCTGAAGATGAAAGGGGAAATAAATGAAAATTTTACTTTTCGATGCCAATG
ATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTTTATTA
TTTAATGTTTTCTAAAATAAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAACAATTA
TTTGTAATAAAAACACTGTTAGTAAT

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FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMIYIGGKYQCHDIDEC SLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGNTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTLRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTD PQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPGLRMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence: amino acids 1-17

N-glycosylation site: amino acids 273-277

Casein kinase II phosphorylation site: amino acids 166-170,
345-349

Tyrosine kinase phosphorylation site: amino acids 199-206

N-myristoylation site: amino acids 109-115, 125-131, 147-153,
191-197, 221-227, 236-242, 421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site: amino acids
104-116, 186-198, 231-243

Cell attachment sequence: amino acids 382-385

EGF-like domain cysteine pattern signature: amino acids 75-87

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FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCTTTAGATTGTGA
 AATGTGGCTCAAGGTCTTCACAACTTTCCTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGA
 AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
 CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
 AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCT
 GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCA
 GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCT
 CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
 CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
 TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
 GCCTGGTGAGGAACCTGTGAGTGAATGGAAAGTGATATCATTATGCCCATCATATATTAT
 GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTTTACTGT
 TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT
 GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
 CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
 CACAGAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT
 ATATCCATGTGTCTTCTTTCCTATGGAAAAAATATCAACCTACAAAGTTATAAAACAGAA
 ACTAGAAGGCAGGCCAGAAACAGAAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
 CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGG
 ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
 GTATGAAGTTATTACGCATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
 GCTAAACAGTACATTTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAGT
 ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
 TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT
 GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
 GGAGAACGAAAGTGACAGGGGTTTCCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
 ATTAGTTCTACTCTACACTTTCACATATCAACACTGAGACTATCCTGTCTCACCTACAAA
 TGTGGAACTTTACATTGTTTCGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG
 TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
 CAAAGTAATAAGGATGGTTGTCACAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC
 AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTA
 TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAAATAAA
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FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPHTMP
 KYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQKIQVTV
 DDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSTSPQNNTLHIA
 PVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTVDLGEAILFDCSA
 DSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNITGRQDETHETVIITSV
 GLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEGRPETEYRKAQTFSGH
 EDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTVYEVIQHIPAQQQDHPE

Signal sequence: amino acids 1-18

Transmembrane domain: amino acids 341-359

N-glycosylation site: amino acids 73-77, 92-96, 117-121,
 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site: amino acids 129-133,
 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site: amino acids 272-280

N-myristoylation site: amino acids 15-21, 19-25, 118-124,
 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 7-18

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FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAGTTCCTGGCAGTCCTGGTGCTGTT
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCTTTGTCCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCTTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTGAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTTCAGTGACAATTTCTGGTCTTTTTTAGAGGTATATTCCAAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAAAACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC
CAACAAAGTTTGATTTTCTCTTGATTTTTTCTTACTTACTATGGGTACATTTTTTTATTTTT
CAAATTGGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT
GTTTCAAAGTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTT
TTGGCCACTTTTTTCAGATTTTACATCATTCTTGCTGAACTTCAACTTGAAATTTGTTTTTT
TTTCTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTGTCTGATGTGAAAAAGCCTTGGA
TTTTACATTTTGAAATTCAAAGAAGCTTAATATAAAAGTTTGCAATCTACTCAGGAAAAAG
CATCTTCTTGATATATGCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACATTTTTATATTTTTTAAAGACAA
ACTTCATATTATCCTGTGTTCTTTCCTGACTGGTAATATTGTGTGGGATTTTCACAGGTAAAA
GTCAGTAGGATGGAACATTTTAGTGTATTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAAGGGGGGAAAATCATAAATAAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT
AAAGAGTTTGGATGTGTAACCTTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAAAA

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FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
 QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
 NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
 ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPSKKLLSESAQPLKKVEEEQEAEEDVSE
 EEAESKEGTNKDFPQNAIRQPSLGPSTLTDKS

Signal sequence: amino acids 1-26

Transmembrane domain: amino acids 182-201

Casein kinase II phosphorylation site: amino acids 68-72,
 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site: amino acids 107-115

N-myristoylation site: amino acids 20-26, 192-198

Amidation site: amino acids 25-29

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FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCCTT
 CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCAGTGGGACAGGCGGATTGGAAGAGCGGG
 AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCAATGAAACTCTGGGTGTCTGC
 ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTG
 GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
 CTTGTGGAGGAAGCCAAGCTTTCAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
 TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGG
 TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
 GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
 GAGGGGAACTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCCTGCTC
 TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
 TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCGTGGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
 CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
 TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCACTGTGCGCCAGCTA
 CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC
 GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTGCAAAT
 TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
 CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
 GTGGTGGCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
 TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCCC
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACTTGACATCCTTTTCTGTCTTCCCCTTCCTGGTC
 CTTACGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTTCTATCAGGCT
 GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
 GTGACTGAAGTCCCAGCCCTTCCATTCAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTGTTTTAT
 GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAAAA

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FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
 NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP
 TDEDEIGAALKMRLQDQTYRLDPGTISRGEPLPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
 LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
 YFEQLLEEEREKTLTNQTEAELATPEGIYERPVLDYLPERDVYESLCRGEGVKLTPRRQKRLF
 CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSEEEIERIKEIAKPKLARATVRDPKTG
 VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
 RRPFDGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYR
 TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVD

Signal sequence: amino acids 1-17

N-glycosylation site: amino acids 115-119, 264-268

Glycosaminoglycan attachment site: amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 477-481

Casein kinase II phosphorylation site: amino acids 43-47,
 72-76, 125-129, 151-155, 165-169, 266-270, 346-350, 365-369,
 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site: amino acids 71-80,
 489-496

N-myristoylation site: amino acids 14-20, 131-137, 171-177,
 446-452

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 8-19

Leucine zipper pattern: amino acids 213-235

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FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAG
TGA AATTGATTGTTTCATTTATTACCGTTTTGGCTGGGGGTTAGTTCCGACACCTTCACAGT
TGAAGAGCAGGCAGAAGGAGTTGTGAAGACAGGACAATCTTCTTGGGGATGCTGGTCCCTGGA
AGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCCAGGTTCTCTGGTTAAAACTGAA
AGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCCCCCTGGGGCAC
CCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGC
TCCCCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGCGGGTTTCCTGGATC
CAGGGGGAGGGAGAAGATCCCTGTGTGCGAGGCTGTAGGGGAGCGAGGAGGGGCCACAGAATCC
AGATTCGAGAGCTCGGCTAGACCAAAGTGATGAAGACTTCAAACCCCGGATTGTCCCCTACT
ACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTCGGTACATCCAGACAGAGCTG
GGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTTGACCTCCCGAGCTACACTGTCCACTTTGGC
CGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGC
GGGGGGCCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGG
CTCATGTGAGAGACCTGCGCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTT
CATCATGCAGGATGACACATATGTGCAGGGCCCCCGCCTGGCAGCCCTTGCTGGCCACCTCA
GCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTGGCGCAGGCGAGCAGGCC
CGGTACTGTCATGGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGCGGCC
ACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCTGACGAGTGGCTTGACGCT
GCCTCATTGACTCTCTGGGCGTCGGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCA
TTTGAACCTGGCCAAAATAGGGACCTGAGAAGGAAGGAGCTCGGCTTTCCTGAGTGCCTT
CGCCGTGCACCCTGTCTCCGAAGGTACCCTCATGTACCGGCTCCACAAACGCTTCAGCGCTC
TGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACCTGCAGGCTCAGATCCGGAACCTGACC
GTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCAC
ACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCT
GTGCAGATGGGGCTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCG
TTGGAGACTGCCCTGGAGCAGCTCAATCGGCGCTATCAGCCCCGCTGCGCTTCAGAAAGCA
GCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCACGGGGCATGGAGTACACCCTGGACC
TGCTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCAGGGTCAGCCTG
CTGCGGCCACTGAGCCGGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGT
GCAGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCCTCGAGGCGT
TTGCAGCCAATGTCTTGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGTCTACGGG
CCACGAGAAGGTGGCCGTGGAGCTCCAGACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGA
GTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCGCTGTGCGAGCAGAGGCCCTT
CCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCCTGTGGACACTCTCTTCTTCCTT
ACCACCGTGTGGACAAGGCCTGGGCCCGAAGTCCTCAACCGCTGTCGCATGAATGCCATCTC
TGGCTGGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTACCCACAGA
GATCACCCCCAGGGCCCCCGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGCTGACCCC
TCCCGGGGGGCTCCTATAGGGGGGAGATTTGACCGGCAGGCTTCTGCGGAGGGCTGCTTCTA
CAACGCTGACTACCTGGCGGCCCGAGCCCGGCTGGCAGGTGAACTGGCAGGCCAGGAAGAGG
AGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCTCCGGTTCTCAGGGCTCCACCTC
TTTCGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCT
CAGTGAAGAACTCTACCACCGCTGCCGCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCC
AGCTGGCTATGGCTCTCTTTGAGCAGGAGCAGGCCAATAGCACTTAGCCCCCTGGGGGCC
TAACCTCATTACCTTTCTTTGTCTGCCTCAGCCCCAGGAAGGGCAAGGCAAGATGGTGGAC
AGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAAACATGTCTTCTGCC

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FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
 QSDEDFKPRIVPYRDPNKPYPYKQVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
 AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWWFFIMQDDTY
 VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
 DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
 GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
 LGWDYFTEQHTFSCADGAPKCPLOQASRADVGDALETALEQLNRRYQPRLRFOKQRLNNGYR
 RFDPARMEYTLDDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPPL
 VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
 TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMAISGWQAFPP
 VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
 RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
 CRLSNLEGLGGRAQLAMALFEQEQA NST

Signal sequence: amino acids 1-15

Transmembrane domain: amino acids 489-507

N-glycosylation site: amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 319-323, 464-468

Casein kinase II phosphorylation site: amino acids 64-68,
 150-154, 322-326, 331-337, 368-372, 385-389, 399-403, 409-413,
 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site: amino acids 736-743

N-myristoylation site: amino acids 19-25, 23-29, 136-142,
 397-403, 441-447, 544-550, 558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 14-25

Cell attachment sequence: amino acids 247-250

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FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACCTACATATCCAA
TACAGCTGTATGTTTCTTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTTTAAATGAGGGTGGTTTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGATTGGTT
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAACCTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

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FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
 LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
 AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
 IVLSVESMKRLNSLLNIPEKCPEQGGMWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
 KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGHIFNDALVEL
 PPNGSDND

Signal sequence: amino acids 1-33

N-glycosylation site: amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 amino acids 319-323, 464-468

Casein kinase II phosphorylation site: amino acids 64-132,
 150-154, 322-326, 331-335, 368-372, 385-389, 399-403, 409-413,
 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site: amino acids 736-743

N-myristoylation site: amino acids 19-25, 23-29, 136-142,
 397-403, 441-447, 544-550, 558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 14-25

Cell attachment sequence: amino acids 247-250

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FIGURE 121

[illegible]

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FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
 FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
 EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCAIMRDSS
 NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence: amino acids 1-42

N-glycosylation site: amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site: amino acids 51-55,
 120-124, 163-167, 175-179, 181-185

N-myristoylation site: amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site: amino
 acids 27-38

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FIGURE 123A

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGG
CGGCCACCGCGACTCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAG
GGGCTGCCTGATAGGGGCTGTAAATCTCAAATCCAGCAATCGAACCCAGTGGTACAGGAAT
TTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCGCAGACAAGTGACCCAGGATCGAG
TGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAATTTCAGGGAGA
CTTGCGGGTTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGA
GAGACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAG
ATTGTGATCGAGTTAACTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGC
TGTACCAGTAGGCAAGATGGCAACACTGCACTGCCAGGAGAGTGAGGGCCACCCCGGCCTC
ACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATTCCAGAGCCAATCCAGATTT
CGCAATTCTTCTTTCCACTTAACTCTGAAACAGGCACTTTGGTGTTCACTGCTGTTACAA
GGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGG
AGCAGGAGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTC
CTTGCTGTACTGGCCCTGATCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCAT
CAACAATAAACAGGATGGAGAAAGTTACAAGAACCCAGGGAAACCAGATGGAGTTAACTACA
TCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTGTGATCTGAGACCCGCGG
TGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAAGGCA
GCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAA
AGTTGACCACTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCCTCAAGATG
GACCCGGTAAATATAACCACAAGGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAA
TCTGTTTTCTGGCCTGATTCCCGCATGAGTATTAGGGTGATCTTAAAGAGTTTGCTCACGTAA
ACGCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTACCACTGGTCGTTGAGCAGCCACGACA
GCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGGCGGGAACCCAG
AAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCT
TAAAGGCTCTGCTGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTT
TGTAACAAACAACCAAAATCAGGAAGGTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGA
ACCCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAACCTTCGTCTTAGGCTAAGTCTGA
AATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTTTACATCTAAAT
TTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAACTGTAAATATATT
GTCATACAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAG
CTACTAGTGTTAAATTGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCA

To Figure 123B

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FIGURE 123B

From Figure 123A

TGGAAGTTTACTGTGATGTTTCCTTTTCTCACACAAGTTTTAGCCTTTTTCACAAGGGAACTC
ATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTTTAAAAATTCCAGTTAAGCAAT
GTTGAAATCAGTTTGCATCTCTTCAAAGAAACCTCTCAGGTTAGCTTTGAACTGCCTCTTC
CTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAC
AGATGCCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGC
TGTCTGCCAGGAGGCCCTGCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTA
CTCACGTGGCCCTTGCTTCATCCAGCACAGCTCTCAGGTGGGCACTGCAGGGACACTGGTGT
CTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCTTTTTGGTTATGGATGGCT
CACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTTGTTAAGAT
TGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTAAAAGA
AAATGGATCCCAGTGTTCCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGC
CATTTCAAACAAACCATGATGGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGG
AGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAGTGAAACGCCTGAATCAAAGCAGTTTTTC
TAATTTTGACTTTAAATTTTTCATCCGCCGAGACACTGCTCCCATTGTGGGGGGACATTA
GCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCTGC
CGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACT
GTGTGCCTGGAGAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTT
TTTATACTTTGACAGCTTTTTTTTAAATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTA
TGTGAAACACTTTGCCGCAGGCCGCTGGCAGAGGCAGGAAATGCTCCAGCAGTGGCTCAGT
GCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTCCTCCATCATTG
CCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCC
TTCTTGGTTGTCATAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAAACCTT
CTACACTAGTGCCATGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGG
AAGTAGCTGCCTATAACTGAGACTAGACGGAAAAGGAATACTCGTGTATTTTAAGATATGAA
TGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCTGCCTTTGGATGGATGTTGCTGT
ACACAGATGCTACAGACTTGTAATAACACACCGTAATTTGGCATTGTGTTAACCTCATTTAT
AAAAGCTTCAAAAAAACCCA

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FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDYDLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Signal peptide: amino acids 1-30

Transmembrane domain: amino acids 243-263

N-glycosylation sites: amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 107-110

Casein kinase II phosphorylation site: amino acids 106-109,
296-299

Tyrosine kinase phosphorylation site: amino acids 69-77

N-myristoylation sites: amino acids 26-31, 215-220, 226-231,
243-248, 244-249, 262-267